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SEQUENCE LISTING

<110> Sheppard, Paul O.
Presnell, Scott R.

<120> MAMMALIAN SECRETED PROTEINS

<130> 00-41

<150> US 60/215,446

<151> 2000-06-30

<160> 329

<170> FastSEQ for Windows Version 3.0

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<211> 453

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<213> Homo sapiens

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<221> CDS

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ctg ctg gtt ttc tcc ctg cct gct ggc cta cat aca gcc ctc aca gca 96
Leu Leu Val Phe Ser Leu Pro Ala Gly Leu His Thr Ala Leu Thr Ala
20 25 30

gcc aga gga ctc ccc aaa ctg ccc aag cac agc cac atc gcc aaa gac 144
Ala Arg Gly Leu Pro Lys Leu Pro Lys His Ser His Ile Ala Lys Asp
35 40 45

acc cat tca tcc ttc cca tct cag ctc cag ggg ctg ctt tcc aaa gca 192
Thr His Ser Ser Phe Pro Ser Gln Leu Gln Gly Leu Leu Ser Lys Ala
50 55 60

Met	Leu	Phe	Pro	Gly	Leu	Thr	Thr	Thr	Leu	Leu	Leu	Leu	Val	Phe	Phe
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Leu	Leu	Val	Phe	Ser	Leu	Pro	Ala	Gly	Leu	His	Thr	Ala	Leu	Thr	Ala
			20					25					30		
Ala	Arg	Gly	Leu	Pro	Lys	Leu	Pro	Lys	His	Ser	His	Ile	Ala	Lys	Asp
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Thr	His	Ser	Ser	Phe	Pro	Ser	Gln	Leu	Gln	Gly	Leu	Leu	Ser	Lys	Ala
	50					55					60				
Thr	Pro	His	Arg	His	Pro	Cys	Asp	Ile	Ala	Gln	Phe	Lys	Thr	Val	Arg
65					70					75					80
Ile	Gln	Glu	Ser	Gln	Gln	Gln	Val	Val	Thr	Lys	Arg	Lys	Phe	Gln	His
				85					90					95	

Phe Thr Ala Ile His Arg Gln Gly Ser Tyr Val Tyr Gln Asp Asn Arg
 100 105 110
 Arg Thr Thr Glu His Arg Pro Ser Ser Ala Val Leu Leu Leu Pro Phe
 115 120 125
 Ala Leu Phe Pro Gln Lys His Val Ile Phe Val Arg Pro Leu Ser Val
 130 135 140
 Val Leu Leu Phe Ala Leu
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gtc cct ccc ctc atc ttc tta ctt tta ccc agc aga tct acc cgt ggg 96
 Val Pro Pro Leu Ile Phe Leu Leu Leu Pro Ser Arg Ser Thr Arg Gly
 20 25 30

cag ccc ttt tcc caa gta cca ggg gag aaa atg gat tca gaa aag gat 144
 Gln Pro Phe Ser Gln Val Pro Gly Glu Lys Met Asp Ser Glu Lys Asp
 35 40 45

ttg tgg gga gag gag ctt cca cac tta ata ctg aaa gag gct ttt cat 192
 Leu Trp Gly Glu Glu Leu Pro His Leu Ile Leu Lys Glu Ala Phe His
 50 55 60

ctg ttt ttc aag cca aca gca gcc cca ttc cca gat tca ctc aag gtc 240
 Leu Phe Phe Lys Pro Thr Ala Ala Pro Phe Pro Asp Ser Leu Lys Val
 65 70 75 80

tcc ctt aca tgt ccc tgg aaa gaa gga ggg tca cat aca aga tgc cag 288
 Ser Leu Thr Cys Pro Trp Lys Glu Gly Gly Ser His Thr Arg Cys Gln
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tgg	gcc	tcc	gtg	agc	gcc	cag	acc	gat	gcc	acc	ccg	gcg	gtg	acg	aca	96
Trp	Ala	Ser	Val	Ser	Ala	Gln	Thr	Asp	Ala	Thr	Pro	Ala	Val	Thr	Thr	
			20					25					30			

gag	ggc	ctc	aac	tcc	acc	gag	gca	gcc	ctg	gcc	acc	ttc	gga	act	ttc	144
Glu	Gly	Leu	Asn	Ser	Thr	Glu	Ala	Ala	Leu	Ala	Thr	Phe	Gly	Thr	Phe	
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ccg	tcg	acc	agg	ccc	ccc	ggg	act	ccc	agg	gct	cca	ggg	ccc	tcc	tcc	192
Pro	Ser	Thr	Arg	Pro	Pro	Gly	Thr	Pro	Arg	Ala	Pro	Gly	Pro	Ser	Ser	
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ggc	ccc	agg	cct	acc	cca	gtc	acg	gac	gtt	gct	gtt	ctc	tgt	gtc	tgt	240
Gly	Pro	Arg	Pro	Thr	Pro	Val	Thr	Asp	Val	Ala	Val	Leu	Cys	Val	Cys	
65					70				75					80		

gac	tta	tcc	cca	gca	cag	tgt	gac	atc	aac	tgc	tgc	tgt	gat	ccc	gac	288
Asp	Leu	Ser	Pro	Ala	Gln	Cys	Asp	Ile	Asn	Cys	Cys	Cys	Asp	Pro	Asp	
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Cys	Ser	Ser	Val	Asp	Phe	Ser	Val	Phe	Ser	Ala	Cys	Ser	Val	Pro	Val	
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gtc	aca	ctt	act	gga	gct	ctc	ccg	tgt	cag	ctc	gta	gca	cag	aag	gtg	384
Val	Thr	Leu	Thr	Gly	Ala	Leu	Pro	Cys	Gln	Leu	Val	Ala	Gln	Lys	Val	
		115					120					125				

aag	agc	ctg	ctg	tgg	ggc	cag	ggc	ttc	cca	gat	tac	gtg	gcc	cct	ttt	432
Lys	Ser	Leu	Leu	Trp	Gly	Gln	Gly	Phe	Pro	Asp	Tyr	Val	Ala	Pro	Phe	
	130				135					140						

gga	aat	tcc	cag	gcc	cag	gac	atg	ctg	gac	tgg	tgc	cca	tcc	act	tca	480
Gly	Asn	Ser	Gln	Ala	Gln	Asp	Met	Leu	Asp	Trp	Cys	Pro	Ser	Thr	Ser	
145					150					155					160	

09093737 06004

528

576

591

[illegible]

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Glu	Gly	Leu	Asn 35	Ser	Thr	Glu	Ala 40	Ala	Leu	Ala	Thr	Phe 45	Gly	Thr	Phe
Pro	Ser	Thr	Arg	Pro	Pro	Gly 55	Thr	Pro	Arg	Ala	Pro	Gly 60	Pro	Ser	Ser
Gly 65	Pro	Arg	Pro	Thr	Pro	Val 70	Thr	Asp	Val	Ala	Val 75	Leu	Cys	Val 80	Cys
Asp	Leu	Ser	Pro	Ala 85	Gln	Cys	Asp	Ile	Asn 90	Cys	Cys	Cys	Asp	Pro 95	Asp
Cys	Ser	Ser	Val 100	Asp	Phe	Ser	Val	Phe 105	Ser	Ala	Cys	Ser	Val 110	Pro	Val
Val	Thr	Leu	Thr 115	Gly	Ala	Leu	Pro 120	Cys	Gln	Leu	Val 125	Ala	Gln	Lys	Val
Lys	Ser	Leu	Leu	Trp	Gly	Gln 135	Gly	Phe	Pro	Asp	Tyr 140	Val	Ala	Pro	Phe
Gly 145	Asn	Ser	Gln	Ala	Gln	Asp 150	Met	Leu	Asp	Trp	Cys 155	Pro	Ser	Thr	Ser
Ser	Pro	Ser	His 165	Ser	Thr	Gly	Arg	Trp	Cys 170	Asp	Glu	Gly	Ser	Arg 175	Gly
Ser	Gln	Leu	Leu	Arg	Arg	Gln	Asp	Gly	Pro	Glu	Trp	Glu	Arg	Gly	Leu

180 185 190
 Asn Leu Gly Tyr
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<220>
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ccg ctg tgg tcc tcc tca ctg cct ggg ctg gac act gct gaa agt aaa 96
 Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
 20 25 30

gcc acc att gca gac ctg atc ctg tct gcg ctg gag aga gcc acc gtc 144
 Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
 35 40 45

ttc cta gaa cag agg ctg cct gaa atc aac ctg gat ggc atg gtg ggg 192
 Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
 50 55 60

gtc cga gtg ctg gaa gcc ctg cgt gaa tgc tct cac tcg gat gtt ctc 240
 Val Arg Val Leu Glu Ala Leu Arg Glu Cys Ser His Ser Asp Val Leu
 65 70 75 80

act cat gtc tcc cca att tct ggc cac ctc tgg atc ttc acc att gtc 288
 Thr His Val Ser Pro Ile Ser Gly His Leu Trp Ile Phe Thr Ile Val
 85 90 95

tcc cac ctc aac aaa gcc act gct agc cca cag gag cag cta aaa agt 336
 Ser His Leu Asn Lys Ala Thr Ala Ser Pro Gln Glu Gln Leu Lys Ser
 100 105 110

gtc cgg gag aag tgg gcc cag gag ccc ctg ctg cag ccg ctg agc ctg 384

00003721.063801

Val	Arg	Glu	Lys	Trp	Ala	Gln	Glu	Pro	Leu	Leu	Gln	Pro	Leu	Ser	Leu		
		115					120					125					
cgc	gtg	ggg	atg	ctg	ggg	gag	aag	ctg	gag	gct	gcc	atc	cag	aga	tcc	432	
Arg	Val	Gly	Met	Leu	Gly	Glu	Lys	Leu	Glu	Ala	Ala	Ile	Gln	Arg	Ser		
	130					135					140						
ctc	cac	tac	ctc	aag	ctg	agt	gat	ccc	aag	tac	cta	aga	gag	ttc	cag	480	
Leu	His	Tyr	Leu	Lys	Leu	Ser	Asp	Pro	Lys	Tyr	Leu	Arg	Glu	Phe	Gln		
145					150					155					160		
ctg	acc	ctc	cag	ccc	ggg	ttt	tgg	aag	ctc	cca	cat	gcc	tgg	atc	cac	528	
Leu	Thr	Leu	Gln	Pro	Gly	Phe	Trp	Lys	Leu	Pro	His	Ala	Trp	Ile	His		
				165					170					175			
act	gat	gcc	tcc	ttg	gtg	tac	ccc	acg	ttc	ggg	ccc	cag	gac	tca	ttc	576	
Thr	Asp	Ala	Ser	Leu	Val	Tyr	Pro	Thr	Phe	Gly	Pro	Gln	Asp	Ser	Phe		
			180					185					190				
tca	gag	gag	aga	agt	gac	gtg	tgc	ctg	gtg	cag	ctg	ctg	gga	acc	ggg	624	
Ser	Glu	Glu	Arg	Ser	Asp	Val	Cys	Leu	Val	Gln	Leu	Leu	Gly	Thr	Gly		
		195					200					205					
acg	gac	agc	agc	gag	ccc	tgc	ggc	ctc	tca	gac	ctc	tgc	agg	agc	ctc	672	
Thr	Asp	Ser	Ser	Glu	Pro	Cys	Gly	Leu	Ser	Asp	Leu	Cys	Arg	Ser	Leu		
	210					215					220						
atg	acc	aag	ccc	ggc	tgc	tca	ggc	tac	tgc	ctg	tcc	cac	caa	ctg	ctc	720	
Met	Thr	Lys	Pro	Gly	Cys	Ser	Gly	Tyr	Cys	Leu	Ser	His	Gln	Leu	Leu		
225					230					235					240		
ttc	ttc	ctc	tgg	gcc	aga	atg	agg	ggg	tgc	aca	cag	gga	cca	ctc	caa	768	
Phe	Phe	Leu	Trp	Ala	Arg	Met	Arg	Gly	Cys	Thr	Gln	Gly	Pro	Leu	Gln		
				245					250					255			
cag	agc	cag	gac	tat	atc	aac	ctc	ttc	tgc	gcc	aac	atg	atg	gac	ttg	816	
Gln	Ser	Gln	Asp	Tyr	Ile	Asn	Leu	Phe	Cys	Ala	Asn	Met	Met	Asp	Leu		
			260					265					270				
aac	cgc	aga	gct	gag	gcc	atc	gga	tac	gcc	tac	cct	acc	cgg	gac	atc	864	
Asn	Arg	Arg	Ala	Glu	Ala	Ile	Gly	Tyr	Ala	Tyr	Pro	Thr	Arg	Asp	Ile		
		275					280					285					

Val 65	Arg	Val	Leu	Glu	Ala	Leu	Arg	Glu	Cys	Ser	His	Ser	Asp	Val	Leu
Thr	His	Val	Ser	Pro	Ile	Ser	Gly	His	Leu	Trp	Ile	Phe	Thr	Ile	Val
Ser	His	Leu	Asn	Lys	Ala	Thr	Ala	Ser	Pro	Gln	Glu	Gln	Leu	Lys	Ser
Val	Arg	Glu	Lys	Trp	Ala	Gln	Glu	Pro	Leu	Leu	Gln	Pro	Leu	Ser	Leu
Arg	Val	Gly	Met	Leu	Gly	Glu	Lys	Leu	Glu	Ala	Ala	Ile	Gln	Arg	Ser
Leu	His	Tyr	Leu	Lys	Leu	Ser	Asp	Pro	Lys	Tyr	Leu	Arg	Glu	Phe	Gln
Leu	Thr	Leu	Gln	Pro	Gly	Phe	Trp	Lys	Leu	Pro	His	Ala	Trp	Ile	His
Thr	Asp	Ala	Ser	Leu	Val	Tyr	Pro	Thr	Phe	Gly	Pro	Gln	Asp	Ser	Phe
Ser	Glu	Glu	Arg	Ser	Asp	Val	Cys	Leu	Val	Gln	Leu	Leu	Gly	Thr	Gly
Thr	Asp	Ser	Ser	Glu	Pro	Cys	Gly	Leu	Ser	Asp	Leu	Cys	Arg	Ser	Leu
Met	Thr	Lys	Pro	Gly	Cys	Ser	Gly	Tyr	Cys	Leu	Ser	His	Gln	Leu	Leu
Phe	Phe	Leu	Trp	Ala	Arg	Met	Arg	Gly	Cys	Thr	Gln	Gly	Pro	Leu	Gln
Gln	Ser	Gln	Asp	Tyr	Ile	Asn	Leu	Phe	Cys	Ala	Asn	Met	Met	Asp	Leu
Asn	Arg	Arg	Ala	Glu	Ala	Ile	Gly	Tyr	Ala	Tyr	Pro	Thr	Arg	Asp	Ile
Phe	Met	Glu	Asn	Ile	Met	Phe	Cys	Gly	Met	Gly	Gly	Phe	Ser	Asp	Phe
Tyr	Lys	Leu	Arg	Trp	Leu	Glu	Ala	Ile	Leu	Ser	Trp	Gln	Lys	Gln	Gln
Glu	Gly	Cys	Phe	Gly	Glu	Pro	Asp	Ala	Glu	Asp	Glu	Glu	Leu	Ser	Lys
Ala	Ile	Gln	Tyr	Gln	Gln	His	Phe	Ser	Arg	Arg	Val	Lys	Arg	Arg	Glu
Lys	Gln	Phe	Pro	Asp	Gly	Cys	Ser	Ser	His	Asn	Thr	Ala	Thr	Ala	Val
Ala	Ala	Leu	Gly	Gly	Phe	Leu	Tyr	Ile	Leu	Ala	Glu	Tyr	Pro	Pro	Ala
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<222> (1)...(555)

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ctg ctt ttt gca ggc acc ccc acc acc cct gag tca atc caa gaa act 144
Leu Leu Phe Ala Gly Thr Pro Thr Thr Pro Glu Ser Ile Gln Glu Thr
35 40 45

gag gtc atc aac cca gga ccg cct agg ggc caa act tct cca gat ccc 192
Glu Val Ile Asn Pro Gly Pro Pro Arg Gly Gln Thr Ser Pro Asp Pro
50 55 60

tac tgg aag act ctg gat ggc agg gcc tgg gaa cct ggt ccc act gaa 240
Tyr Trp Lys Thr Leu Asp Gly Arg Ala Trp Glu Pro Gly Pro Thr Glu
65 70 75 80

acc aag gaa ctg gag gac aac gag gtc atc ccc agg agg atc tca ctc 288
Thr Lys Glu Leu Glu Asp Asn Glu Val Ile Pro Arg Arg Ile Ser Leu
85 90 95

Ser Ala Gly Asp Gln Asp Val Ser Asn Lys Ala Pro Met Ser Asn Thr
 100 105 110
 Ala Gln Gly Ser Asn Ile Phe Glu Arg Met Glu Val Val Ala Val Leu
 115 120 125
 Ile Val Asp Ser Ile Ala Gly Ile Leu Ser Ala Val Phe Leu Ile Leu
 130 135 140
 Leu Leu Val Asn His Met Lys Lys Asp Glu Gly Arg Asn Asp Leu Ser
 145 150 155 160
 Arg Lys Pro Ile Tyr Lys Lys Ala Pro Ser Lys Glu Leu Leu Arg Phe
 165 170 175
 Phe Tyr Glu His Trp Phe Gly Leu
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<210> 15
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

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1 5 10 15	
tgg ctg gcc tgg gcc ccg gct gcc tct gcc tac agt gcc atc cac gct	96
Trp Leu Ala Trp Ala Pro Ala Ala Ser Ala Tyr Ser Ala Ile His Ala	
20 25 30	
agg gaa cag ctg tcc cca caa gaa cca tgt ggt cca tgt ctg ggc agt	144
Arg Glu Gln Leu Ser Pro Gln Glu Pro Cys Gly Pro Cys Leu Gly Ser	
35 40 45	
gac cgc ctc act tgc agc caa ccc cac act ctt cag tgg tgc cga ggt	192
Asp Arg Leu Thr Cys Ser Gln Pro His Thr Leu Gln Trp Cys Arg Gly	
50 55 60	
cct gtg gca gac tca gcc aat ccc agt gtg gac ttg act cgg tct tgg	240
Pro Val Ala Asp Ser Ala Asn Pro Ser Val Asp Leu Thr Arg Ser Trp	
65 70 75 80	

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<213> Homo sapiens

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1		5			10				15							
ctc	cct	tct	tgg	cct	ccc	aat	gtg	gtg	gta	tta	cag	gcc	ggg	cct	cca	96
Leu	Pro	Ser	Trp	Pro	Pro	Asn	Val	Val	Val	Leu	Gln	Ala	Gly	Pro	Pro	
			20		25				30							
ctt	tct	cat	gtc	acc	cac	tct	gct	att	act	cca	tgc	tcc	cat	cct	tcc	144
Leu	Ser	His	Val	Thr	His	Ser	Ala	Ile	Thr	Pro	Cys	Ser	His	Pro	Ser	
35			40				45									
tac	gtc	ctt	act	ttc	acc	cag	gat	gag	aaa	gtg	ccc	cac	cgt	gtc	cag	192
Tyr	Val	Leu	Thr	Phe	Thr	Gln	Asp	Glu	Lys	Val	Pro	His	Arg	Val	Gln	
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1			5			10			15							
gca	cag	gcc	ttt	cca	caa	aca	gac	atc	agt	atc	agt	cca	gcc	ctg	cca	96
Ala	Gln	Ala	Phe	Pro	Gln	Thr	Asp	Ile	Ser	Ile	Ser	Pro	Ala	Leu	Pro	
20			25			30										
gag	ctg	ccc	ctg	cct	tcc	ctg	tgc	ccc	ctg	ttc	tgg	atg	gag	ttc	aaa	144
Glu	Leu	Pro	Leu	Pro	Ser	Leu	Cys	Pro	Leu	Phe	Trp	Met	Glu	Phe	Lys	
35			40			45										
ggc	cac	tgc	tat	cga	ttc	ttc	cct	ctc	aat	aag	acc	tgg	gct	gag	gcc	192
Gly	His	Cys	Tyr	Arg	Phe	Phe	Pro	Leu	Asn	Lys	Thr	Trp	Ala	Glu	Ala	
50			55			60										
gac	ctc	tac	tgt	tct	gag	ttc	tct	gtg	ggc	agg	aag	tcc	gcc	aag	ctg	240
Asp	Leu	Tyr	Cys	Ser	Glu	Phe	Ser	Val	Gly	Arg	Lys	Ser	Ala	Lys	Leu	
65			70			75			80							
gcc	tcc	atc	cac	agc	tgg	gag	gag	aat	gtc	ttt	gta	tat	gac	ctc	gtg	288
Ala	Ser	Ile	His	Ser	Trp	Glu	Glu	Asn	Val	Phe	Val	Tyr	Asp	Leu	Val	
85			90			95										

Met	Gln	Arg	Trp	Thr	Leu	Trp	Ala	Ala	Ala	Phe	Leu	Thr	Leu	His	Ser
1				5				10						15	
Ala	Gln	Ala	Phe	Pro	Gln	Thr	Asp	Ile	Ser	Ile	Ser	Pro	Ala	Leu	Pro
			20					25					30		
Glu	Leu	Pro	Leu	Pro	Ser	Leu	Cys	Pro	Leu	Phe	Trp	Met	Glu	Phe	Lys
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Gly	His	Cys	Tyr	Arg	Phe	Phe	Pro	Leu	Asn	Lys	Thr	Trp	Ala	Glu	Ala
	50					55					60				
Asp	Leu	Tyr	Cys	Ser	Glu	Phe	Ser	Val	Gly	Arg	Lys	Ser	Ala	Lys	Leu
65					70					75					80
Ala	Ser	Ile	His	Ser	Trp	Glu	Glu	Asn	Val	Phe	Val	Tyr	Asp	Leu	Val
				85					90					95	
Asn	Ser	Cys	Val	Pro	Gly	Ile	Pro	Ala	Asp	Val	Trp	Thr	Gly	Leu	His
			100					105					110		
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<212> DNA
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1			5			10			15							
tgc	agc	caa	ccc	tgc	cag	agt	ccc	caa	ggg	gcc	cta	gcc	atg	ctg	ccg	96
Cys	Ser	Gln	Pro	Cys	Gln	Ser	Pro	Gln	Gly	Ala	Leu	Ala	Met	Leu	Pro	
20			25			30										
ctt	gtg	cta	gcc	ttc	atc	agt	gaa	atc	tca	gcc	caa	cca	aac	cag	ttt	144
Leu	Val	Leu	Ala	Phe	Ile	Ser	Glu	Ile	Ser	Ala	Gln	Pro	Asn	Gln	Phe	
35			40			45										
cag	ggg	gcc	agc	tca	gtg	aca	ttc	att	tcc	aca	ctt	ttg	ttg	aac	ccg	192
Gln	Gly	Ala	Ser	Ser	Val	Thr	Phe	Ile	Ser	Thr	Leu	Leu	Leu	Asn	Pro	
50			55			60										
acc	ttc	act	aag	cac	tgg	ctc	tgc	acc	agg	agt	gtg	cgg	ggc	cct	ggc	240
Thr	Phe	Thr	Lys	His	Trp	Leu	Cys	Thr	Arg	Ser	Val	Arg	Gly	Pro	Gly	
65			70			75			80							
atg	cag	ggg	ccc	cag	gcc	agc	ccc	agc	cct	gct	ctg	gag	ctt	atg	atg	288
Met	Gln	Gly	Pro	Gln	Ala	Ser	Pro	Ser	Pro	Ala	Leu	Glu	Leu	Met	Met	
85			90			95										
gaa	ctt	aac	cag	aag	aag	cta	agg	aag	aga	aga	gag	gag	agg	aga	gag	336
Glu	Leu	Asn	Gln	Lys	Lys	Leu	Arg	Lys	Arg	Arg	Glu	Glu	Arg	Arg	Glu	

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<210> 22
<211> 176
<212> PRT
<213> Homo sapiens

<400> 22
Met Pro Arg Val Met Ala Trp Arg Tyr Trp Val His Thr Asp Gly Cys
 1          5          10          15
Cys Ser Gln Pro Cys Gln Ser Pro Gln Gly Ala Leu Ala Met Leu Pro
          20          25          30
Leu Val Leu Ala Phe Ile Ser Glu Ile Ser Ala Gln Pro Asn Gln Phe
          35          40          45
Gln Gly Ala Ser Ser Val Thr Phe Ile Ser Thr Leu Leu Leu Asn Pro
          50          55          60
Thr Phe Thr Lys His Trp Leu Cys Thr Arg Ser Val Arg Gly Pro Gly
65          70          75          80
Met Gln Gly Pro Gln Ala Ser Pro Ser Pro Ala Leu Glu Leu Met Met
          85          90          95
Glu Leu Asn Gln Lys Lys Leu Arg Lys Arg Arg Glu Glu Arg Arg Glu
          100          105          110

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<400> 22															
Met	Pro	Arg	Val	Met	Ala	Trp	Arg	Tyr	Trp	Val	His	Thr	Asp	Gly	Cys
1				5					10					15	
Cys	Ser	Gln	Pro	Cys	Gln	Ser	Pro	Gln	Gly	Ala	Leu	Ala	Met	Leu	Pro
			20					25					30		
Leu	Val	Leu	Ala	Phe	Ile	Ser	Glu	Ile	Ser	Ala	Gln	Pro	Asn	Gln	Phe
		35					40					45			
Gln	Gly	Ala	Ser	Ser	Val	Thr	Phe	Ile	Ser	Thr	Leu	Leu	Leu	Asn	Pro
	50					55					60				
Thr	Phe	Thr	Lys	His	Trp	Leu	Cys	Thr	Arg	Ser	Val	Arg	Gly	Pro	Gly
65					70					75					80
Met	Gln	Gly	Pro	Gln	Ala	Ser	Pro	Ser	Pro	Ala	Leu	Glu	Leu	Met	Met
				85					90					95	
Glu	Leu	Asn	Gln	Lys	Lys	Leu	Arg	Lys	Arg	Arg	Glu	Glu	Arg	Arg	Glu
			100					105					110		

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<210> 23
<211> 282
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(282)
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<400> 23

gcc ctg ggg gca tcc gca gga ggg agg cat gct ttt ggg tac cga cac 96
Ala Leu Gly Ala Ser Ala Gly Gly Arg His Ala Phe Gly Tyr Arg His
20 25 30

atg ttc ctc cag gag gag tgg tgg aaa gga gga atc ctt tgg cct cca 144
Met Phe Leu Gln Glu Glu Trp Trp Lys Gly Gly Ile Leu Trp Pro Pro
35 40 45

acc ctg gaa gaa ggg tcc atg tgg gag gaa aca gct cac agg tca tca 192
Thr Leu Glu Glu Gly Ser Met Trp Glu Glu Thr Ala His Arg Ser Ser
50 55 60

atg aga cat cgg aga gag ccg cta ggt gtt gtg gca gat gag gca gtg 240
Met Arg His Arg Arg Glu Pro Leu Gly Val Val Ala Asp Glu Ala Val
65 70 75 80

cct cca cgt gtg ctc atg ggc act ccc ggt cat gaa gag tga 282
Pro Pro Arg Val Leu Met Gly Thr Pro Gly His Glu Glu *
85 90

<210> 24
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Ala Arg Cys Pro Leu Leu Leu Phe Pro Leu Pro Leu Val Pro Met
 1 5 10 15
 Ala Leu Gly Ala Ser Ala Gly Gly Arg His Ala Phe Gly Tyr Arg His
 20 25 30
 Met Phe Leu Gln Glu Glu Trp Trp Lys Gly Gly Ile Leu Trp Pro Pro
 35 40 45
 Thr Leu Glu Glu Gly Ser Met Trp Glu Glu Thr Ala His Arg Ser Ser
 50 55 60
 Met Arg His Arg Arg Glu Pro Leu Gly Val Val Ala Asp Glu Ala Val
 65 70 75 80
 Pro Pro Arg Val Leu Met Gly Thr Pro Gly His Glu Glu
 85 90

<210> 25
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(372)

<400> 25
 atg ccc cct gac ccc aag gca ctg ctc tgc ctc aac ctc ccc cac ttc 48
 Met Pro Pro Asp Pro Lys Ala Leu Leu Cys Leu Asn Leu Pro His Phe
 1 5 10 15
 gcc ctg tgc cag ccc tgg gta ccc tcc ctg cag gcc gcg tcc ctc gcc 96
 Ala Leu Cys Gln Pro Trp Val Pro Ser Leu Gln Ala Ala Ser Leu Ala
 20 25 30
 acc tgg cct cct gtc ttc tgg aac tca ggc cct gcc ccc tgc tcc cag 144
 Thr Trp Pro Pro Val Phe Trp Asn Ser Gly Pro Ala Pro Cys Ser Gln
 35 40 45
 cct cca atg ccc acg tcc aac agg act ctg ctt ctc agc ccc acc tca 192

<220>
<221> CDS
<222> (1)...(657)

atg gag aca gag cct tca aag gcc aga gcc aat gac cca gga tca gct 48
Met Glu Thr Glu Pro Ser Lys Ala Arg Ala Asn Asp Pro Gly Ser Ala
1 5 10 15

gca gag ggg ctc agc ctg ttg ctg ctt ccc ttg ctc ctg gtt caa gct 96
Ala Glu Gly Leu Ser Leu Leu Leu Leu Pro Leu Leu Leu Val Gln Ala
20 25 30

ggt gtc tgg gga ttc cca agg ccc cca ggg agg ccc cag ctg agc ctg 144
Gly Val Trp Gly Phe Pro Arg Pro Pro Gly Arg Pro Gln Leu Ser Leu
35 40 45

cag gag ctg cgg agg gag ttc aca gtc agc ctg cat ctc gcc agg aag 192
Gln Glu Leu Arg Arg Glu Phe Thr Val Ser Leu His Leu Ala Arg Lys
50 55 60

ctg ctc tcc gag gtt cgg ggc cag gcc cac cgc ttt gac ccg gag cgt 240
Leu Leu Ser Glu Val Arg Gly Gln Ala His Arg Phe Asp Pro Glu Arg
65 70 75 80

ctc tgc ttc atc tcc acc acg ctt cag ccc ttc cat gcc ctg ctg gga 288
Leu Cys Phe Ile Ser Thr Thr Leu Gln Pro Phe His Ala Leu Leu Gly
85 90 95

ggg ctg ggg acc cag ggc cgc tgg acc aac atg gag agg atg cag ctg 336
Gly Leu Gly Thr Gln Gly Arg Trp Thr Asn Met Glu Arg Met Gln Leu
100 105 110

tgg gcc atg agg ctg gac ctc cgc gat ctg cag cgg cac ctc cgc ttc 384
Trp Ala Met Arg Leu Asp Leu Arg Asp Leu Gln Arg His Leu Arg Phe
115 120 125

cag gtg ctg gct gca gga ttc aac ctc ccg gag gag gag gag gag gaa 432

Gln Val Leu Ala Ala Gly Phe Asn Leu Pro Glu Glu Glu Glu Glu
 130 135 140
 gag gag gag gag gag gag gag agg aag ggg ctg ctc cca ggg gca ctg 480
 Glu Glu Glu Glu Glu Glu Glu Arg Lys Gly Leu Leu Pro Gly Ala Leu
 145 150 155 160
 ggc agc gcc tta cag ggc ccg gcc cag gtg tcc tgg ccc cag ctc ctc 528
 Gly Ser Ala Leu Gln Gly Pro Ala Gln Val Ser Trp Pro Gln Leu Leu
 165 170 175
 tcc acc tac cgc ctg ctg cac tcc ttg gag ctc gtc tta tct cgg gcc 576
 Ser Thr Tyr Arg Leu Leu His Ser Leu Glu Leu Val Leu Ser Arg Ala
 180 185 190
 gtg cgg gag ttg ctg ctg ctg tcc aag gct ggg cac tca gtc tgg ccc 624
 Val Arg Glu Leu Leu Leu Leu Ser Lys Ala Gly His Ser Val Trp Pro
 195 200 205
 ttg ggg ttc cca aca ttg agc ccc cag ccc tga 657
 Leu Gly Phe Pro Thr Leu Ser Pro Gln Pro *
 210 215

<210> 28
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Glu Thr Glu Pro Ser Lys Ala Arg Ala Asn Asp Pro Gly Ser Ala
 1 5 10 15
 Ala Glu Gly Leu Ser Leu Leu Leu Leu Pro Leu Leu Leu Val Gln Ala
 20 25 30
 Gly Val Trp Gly Phe Pro Arg Pro Pro Gly Arg Pro Gln Leu Ser Leu
 35 40 45
 Gln Glu Leu Arg Arg Glu Phe Thr Val Ser Leu His Leu Ala Arg Lys
 50 55 60
 Leu Leu Ser Glu Val Arg Gly Gln Ala His Arg Phe Asp Pro Glu Arg
 65 70 75 80
 Leu Cys Phe Ile Ser Thr Thr Leu Gln Pro Phe His Ala Leu Leu Gly
 85 90 95
 Gly Leu Gly Thr Gln Gly Arg Trp Thr Asn Met Glu Arg Met Gln Leu

100 105 110
 Trp Ala Met Arg Leu Asp Leu Arg Asp Leu Gln Arg His Leu Arg Phe
 115 120 125
 Gln Val Leu Ala Ala Gly Phe Asn Leu Pro Glu Glu Glu Glu Glu Glu
 130 135 140
 Glu Glu Glu Glu Glu Glu Glu Arg Lys Gly Leu Leu Pro Gly Ala Leu
 145 150 155 160
 Gly Ser Ala Leu Gln Gly Pro Ala Gln Val Ser Trp Pro Gln Leu Leu
 165 170 175
 Ser Thr Tyr Arg Leu Leu His Ser Leu Glu Leu Val Leu Ser Arg Ala
 180 185 190
 Val Arg Glu Leu Leu Leu Leu Ser Lys Ala Gly His Ser Val Trp Pro
 195 200 205
 Leu Gly Phe Pro Thr Leu Ser Pro Gln Pro
 210 215

<210> 29
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(533)

<400> 29

atg cac gtt cca gtg ata aag ctg tgc acg gca gcc atg gct atc cag 48
 Met His Val Pro Val Ile Lys Leu Cys Thr Ala Ala Met Ala Ile Gln
 1 5 10 15

ctg gcc cag ccc aac aga gat ctg tgg ttc ctc act tgc ctg cac ctt 96
 Leu Ala Gln Pro Asn Arg Asp Leu Trp Phe Leu Thr Cys Leu His Leu
 20 25 30

ctc tgc ctt ctc ctc tta cca tca cct cca ata tca gca ggt cct ggt 144
 Leu Cys Leu Leu Leu Leu Pro Ser Pro Pro Ile Ser Ala Gly Pro Gly
 35 40 45

cct tct ctg cct tct ccc ctc acc atc atg tcc aat atc agc agc tgc 192
 Pro Ser Leu Pro Ser Pro Leu Thr Ile Met Ser Asn Ile Ser Ser Cys
 50 55 60

cag agc ctg gcc cca cca tca tcc tct ccc agc tgg aca ggt gtt cct 240

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<210> 30
<211> 177
<212> PRT
<213> Homo sapiens
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<400> 30
Met His Val Pro Val Ile Lys Leu Cys Thr Ala Ala Met Ala Ile Gln
1 5 10 15
Leu Ala Gln Pro Asn Arg Asp Leu Trp Phe Leu Thr Cys Leu His Leu
20 25 30
Leu Cys Leu Leu Leu Leu Pro Ser Pro Pro Ile Ser Ala Gly Pro Gly

35 40 45
 Pro Ser Leu Pro Ser Pro Leu Thr Ile Met Ser Asn Ile Ser Ser Cys
 50 55 60
 Gln Ser Leu Ala Pro Pro Ser Ser Ser Pro Ser Trp Thr Gly Val Pro
 65 70 75 80
 Ala Phe Gln Val Gly Ser Gln Pro Pro Pro Leu Glu Val Asp Leu Gln
 85 90 95
 Glu Leu Phe Gly Glu Asp Lys Arg Leu Leu Lys Val Glu His Leu Cys
 100 105 110
 Cys Cys Gly Tyr Val Pro Val Thr Ser Ile Gln Pro Ile Trp Gly Ala
 115 120 125
 His Leu Leu Cys Leu Lys Gly Lys Phe Asn Thr Val Lys Phe Val Leu
 130 135 140
 Gln Arg Ser Gln Ile Val Trp Ala Gln Ser Ser Thr Arg Gly Leu Thr
 145 150 155 160
 Thr Asn Ser Arg Ile Leu Pro Pro Leu Tyr Leu Pro Cys Met Leu Leu
 165 170 175
 Ala

<210> 31
 <211> 525
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(525)

<400> 31

atg gga gtc tca ctg gat cag gag cac agc aga cac cct gct gga tct 48
 Met Gly Val Ser Leu Asp Gln Glu His Ser Arg His Pro Ala Gly Ser
 1 5 10 15

gga ggt atg gga gtc agc ggc agg tct gcg aca gtg gca aac agc agt 96
 Gly Gly Met Gly Val Ser Gly Arg Ser Ala Thr Val Ala Asn Ser Ser
 20 25 30

ggt gga tgg atc ttt ggg gtg ttg ctt ttc tca ccg gaa acc tct gca 144
 Gly Gly Trp Ile Phe Gly Val Leu Leu Phe Ser Pro Glu Thr Ser Ala
 35 40 45

gcc agt ggc atc ttt gcc caa gtt cat gtc ctg tgt cca gga aga atg 192

Ala Ser Gly Ile Phe Ala Gln Val His Val Leu Cys Pro Gly Arg Met
 50 55 60

agg tat gca gac aag tgg agg agg gaa gga agt gca tgc cga ttg gtc 240
 Arg Tyr Ala Asp Lys Trp Arg Arg Glu Gly Ser Ala Cys Arg Leu Val
 65 70 75 80

cat agg cag cca tgg gct gct gga aaa ggc acc aca agt ccc cac tct 288
 His Arg Gln Pro Trp Ala Ala Gly Lys Gly Thr Thr Ser Pro His Ser
 85 90 95

gga cag tgg aat agc agc cca acc ccc agc ctt caa gac ctc cct ggc 336
 Gly Gln Trp Asn Ser Ser Pro Thr Pro Ser Leu Gln Asp Leu Pro Gly
 100 105 110

ctg aag aac aga aat ttg gct gct atg aaa ctt gac aag ccg atc ccc 384
 Leu Lys Asn Arg Asn Leu Ala Ala Met Lys Leu Asp Lys Pro Ile Pro
 115 120 125

agc cca tca ctt agg cac aat ctc ttt gag att tta aga gcg cgc cag 432
 Ser Pro Ser Leu Arg His Asn Leu Phe Glu Ile Leu Arg Ala Arg Gln
 130 135 140

cca tgc ctg tac gcc tgc aac tcg aaa ctg cgc att cga gga cca gca 480
 Pro Cys Leu Tyr Ala Cys Asn Ser Lys Leu Arg Ile Arg Gly Pro Ala
 145 150 155 160

ggg ccc cta gag agc atg ggc ttg agg tgt cgt tcc ccg gag tga 525
 Gly Pro Leu Glu Ser Met Gly Leu Arg Cys Arg Ser Pro Glu *
 165 170

<210> 32

<211> 174

<212> PRT

<213> Homo sapiens

<400> 32

Met Gly Val Ser Leu Asp Gln Glu His Ser Arg His Pro Ala Gly Ser
 1 5 10 15

Gly Gly Met Gly Val Ser Gly Arg Ser Ala Thr Val Ala Asn Ser Ser
 20 25 30

Gly Gly Trp Ile Phe Gly Val Leu Leu Phe Ser Pro Glu Thr Ser Ala

F08999.2E2E660

35 40 45
 Ala Ser Gly Ile Phe Ala Gln Val His Val Leu Cys Pro Gly Arg Met
 50 55 60
 Arg Tyr Ala Asp Lys Trp Arg Arg Glu Gly Ser Ala Cys Arg Leu Val
 65 70 75 80
 His Arg Gln Pro Trp Ala Ala Gly Lys Gly Thr Thr Ser Pro His Ser
 85 90 95
 Gly Gln Trp Asn Ser Ser Pro Thr Pro Ser Leu Gln Asp Leu Pro Gly
 100 105 110
 Leu Lys Asn Arg Asn Leu Ala Ala Met Lys Leu Asp Lys Pro Ile Pro
 115 120 125
 Ser Pro Ser Leu Arg His Asn Leu Phe Glu Ile Leu Arg Ala Arg Gln
 130 135 140
 Pro Cys Leu Tyr Ala Cys Asn Ser Lys Leu Arg Ile Arg Gly Pro Ala
 145 150 155 160
 Gly Pro Leu Glu Ser Met Gly Leu Arg Cys Arg Ser Pro Glu
 165 170

<210> 33
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(369)

<400> 33
 atg cgc tcc ctg cat aac gcg cgg cac gcc tcc ttc gct caa ctt ggc 48
 Met Arg Ser Leu His Asn Ala Arg His Ala Ser Phe Ala Gln Leu Gly
 1 5 10 15
 cgt atg ttg att gtc agc atc aac aag ctc cta atg cca cct tta aaa 96
 Arg Met Leu Ile Val Ser Ile Asn Lys Leu Leu Met Pro Pro Leu Lys
 20 25 30
 gtg tct ata tct ctt tta aga tta tta cct cct aca ttt gct gtg ctc 144
 Val Ser Ile Ser Leu Leu Arg Leu Leu Pro Pro Thr Phe Ala Val Leu
 35 40 45
 ttt gta tac aac tcc cgt ttc cgc gct gct tct tac atg caa cac ctc 192
 Phe Val Tyr Asn Ser Arg Phe Arg Ala Ala Ser Tyr Met Gln His Leu
 50 55 60

1033330 4444440

<210> 35
<211> 1148

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1148)

<400> 35

atg	gag	ccc	ctg	cgc	gcg	ccc	gcg	ctg	cgc	cgc	ctg	ctg	ccg	ccg	ctg	48
Met	Glu	Pro	Leu	Arg	Ala	Pro	Ala	Leu	Arg	Arg	Leu	Leu	Pro	Pro	Leu	
1				5					10					15		

ctg	ctc	ctg	ctg	ctg	tca	ctg	ccc	ccc	cgc	gcc	cgg	gcc	aag	tac	gtg	96
Leu	Leu	Leu	Leu	Leu	Ser	Leu	Pro	Pro	Arg	Ala	Arg	Ala	Lys	Tyr	Val	
				20				25						30		

cgg	ggc	aac	ctc	agt	tcc	aag	gag	gac	tgg	gtg	ttc	ctg	aca	aga	ttt	144
Arg	Gly	Asn	Leu	Ser	Ser	Lys	Glu	Asp	Trp	Val	Phe	Leu	Thr	Arg	Phe	
		35					40					45				

tgt	ttc	ctc	tcg	gat	tac	ggc	cga	ctg	gac	ttc	cgt	ttc	cgc	tac	cct	192
Cys	Phe	Leu	Ser	Asp	Tyr	Gly	Arg	Leu	Asp	Phe	Arg	Phe	Arg	Tyr	Pro	
	50					55					60					

gag	gcc	aag	tgc	tgt	cag	aac	atc	ctc	ctc	tat	ttt	gat	gac	cca	tcc	240
Glu	Ala	Lys	Cys	Cys	Gln	Asn	Ile	Leu	Leu	Tyr	Phe	Asp	Asp	Pro	Ser	
65					70					75					80	

cag	tgg	cca	gcc	gtg	tac	aag	gca	ggg	gac	aag	gac	tgc	ctg	gcc	aag	288
Gln	Trp	Pro	Ala	Val	Tyr	Lys	Ala	Gly	Asp	Lys	Asp	Cys	Leu	Ala	Lys	
				85					90						95	

gag	tca	gtg	atc	cgg	ccg	gag	aac	aac	cag	gtc	atc	aac	ctc	acc	acc	336
Glu	Ser	Val	Ile	Arg	Pro	Glu	Asn	Asn	Gln	Val	Ile	Asn	Leu	Thr	Thr	
			100					105					110			

cag	tat	gcc	tgg	tcc	ggc	tgt	cag	gtg	gta	tca	gag	gag	gga	acc	cgc	384
Gln	Tyr	Ala	Trp	Ser	Gly	Cys	Gln	Val	Val	Ser	Glu	Glu	Gly	Thr	Arg	
		115				120						125				

tac	ctg	agc	tgc	tcc	agt	ggc	cgc	agc	ttc	cgc	tca	gtg	cgt	gaa	cgg	432
Tyr	Leu	Ser	Cys	Ser	Ser	Gly	Arg	Ser	Phe	Arg	Ser	Val	Arg	Glu	Arg	
	130					135					140					

tgg tgg tat att gcg ctc agc aag tgt ggg ggt gat gga ttg cag ctg Trp Trp Tyr Ile Ala Leu Ser Lys Cys Gly Gly Asp Gly Leu Gln Leu 145 150 155 160	480
gag tat gag atg gtc ctc acc aat ggc aag tcc ttc tgg aca cga cac Glu Tyr Glu Met Val Leu Thr Asn Gly Lys Ser Phe Trp Thr Arg His 165 170 175	528
ttc tcc gct gat gag ttt ggg atc ctg gag aca gat gtg acc ttc ctc Phe Ser Ala Asp Glu Phe Gly Ile Leu Glu Thr Asp Val Thr Phe Leu 180 185 190	576
ctc atc ttc atc ctc atc ttc ttc ctc tct tgt tac ttt gga tat ttg Leu Ile Phe Ile Leu Ile Phe Phe Leu Ser Cys Tyr Phe Gly Tyr Leu 195 200 205	624
ctg aaa ggt cgt cag ttg ctc cac aca act tat aaa atg ttc atg gcc Leu Lys Gly Arg Gln Leu Leu His Thr Thr Tyr Lys Met Phe Met Ala 210 215 220	672
gca gca gga gta gag gtc ctg agc ctc cta ttt ttc tgc atc tac tgg Ala Ala Gly Val Glu Val Leu Ser Leu Leu Phe Phe Cys Ile Tyr Trp 225 230 235 240	720
ggt caa tat gcc acc gat ggc att ggc aac gag agt gtg aag atc ttg Gly Gln Tyr Ala Thr Asp Gly Ile Gly Asn Glu Ser Val Lys Ile Leu 245 250 255	768
gcc aag ctg ctc ttc tcc tcc agc ttc ctc atc ttc ctg ctg atg ctt Ala Lys Leu Leu Phe Ser Ser Ser Phe Leu Ile Phe Leu Leu Met Leu 260 265 270	816
atc ctc ctg ggg aag gga ttc acg gtg aca cgg tgc ccg ggc agg gcg Ile Leu Leu Gly Lys Gly Phe Thr Val Thr Arg Cys Pro Gly Arg Ala 275 280 285	864
tgc tcg tgg ggc ggc tgg ggc cgc atc agc cac gcg ggc tcc gtg aag Cys Ser Trp Gly Gly Trp Gly Arg Ile Ser His Ala Gly Ser Val Lys 290 295 300	912
ttg tct gtc tac atg acc ctg tac acg ctc acc cat gtg gtg ctg ctc Leu Ser Val Tyr Met Thr Leu Tyr Thr Leu Thr His Val Val Leu Leu	960


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<210> 36
<211> 382
<212> PRT
<213> Homo sapiens

<400> 36
Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu
1          5          10          15
Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
          20          25          30
Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
          35          40          45
Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
          50          55          60
Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser
65          70          75          80
Gln Trp Pro Ala Val Tyr Lys Ala Gly Asp Lys Asp Cys Leu Ala Lys
          85          90          95
Glu Ser Val Ile Arg Pro Glu Asn Asn Gln Val Ile Asn Leu Thr Thr
          100          105          110
Gln Tyr Ala Trp Ser Gly Cys Gln Val Val Ser Glu Glu Gly Thr Arg
          115          120          125
Tyr Leu Ser Cys Ser Ser Gly Arg Ser Phe Arg Ser Val Arg Glu Arg
          130          135          140

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<210> 36
<211> 382
<212> PRT
<213> Homo sapiens
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Trp Trp Tyr Ile Ala Leu Ser Lys Cys Gly Gly Asp Gly Leu Gln Leu
 145 150 155 160
 Glu Tyr Glu Met Val Leu Thr Asn Gly Lys Ser Phe Trp Thr Arg His
 165 170 175
 Phe Ser Ala Asp Glu Phe Gly Ile Leu Glu Thr Asp Val Thr Phe Leu
 180 185 190
 Leu Ile Phe Ile Leu Ile Phe Phe Leu Ser Cys Tyr Phe Gly Tyr Leu
 195 200 205
 Leu Lys Gly Arg Gln Leu Leu His Thr Thr Tyr Lys Met Phe Met Ala
 210 215 220
 Ala Ala Gly Val Glu Val Leu Ser Leu Leu Phe Phe Cys Ile Tyr Trp
 225 230 235 240
 Gly Gln Tyr Ala Thr Asp Gly Ile Gly Asn Glu Ser Val Lys Ile Leu
 245 250 255
 Ala Lys Leu Leu Phe Ser Ser Ser Phe Leu Ile Phe Leu Leu Met Leu
 260 265 270
 Ile Leu Leu Gly Lys Gly Phe Thr Val Thr Arg Cys Pro Gly Arg Ala
 275 280 285
 Cys Ser Trp Gly Gly Trp Gly Arg Ile Ser His Ala Gly Ser Val Lys
 290 295 300
 Leu Ser Val Tyr Met Thr Leu Tyr Thr Leu Thr His Val Val Leu Leu
 305 310 315 320
 Ile Tyr Glu Ala Glu Phe Phe Asp Pro Gly Gln Val Leu Tyr Thr Tyr
 325 330 335
 Glu Ser Pro Ala Gly Tyr Gly Leu Ile Gly Leu Gln Val Ala Ala Tyr
 340 345 350
 Val Trp Phe Cys Tyr Ala Val Leu Val Ser Leu Arg His Phe Pro Glu
 355 360 365
 Lys Gln Pro Phe Tyr Val Pro Phe Phe Ala Ala Tyr Thr Leu
 370 375 380

<210> 37

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(333)

<400> 37

atg tcg gtg gtt gag gtg caa ggc ctc gtg tgt tat gcg agg cgt ccg
 Met Ser Val Val Glu Val Gln Gly Leu Val Cys Tyr Ala Arg Arg Pro

1	5	10	15	
ctg ata ctt cct ctg ctg ctc ttc tgg tgc ttg agc ggg tct agt cgt				96
Leu Ile Leu Pro Leu Leu Leu Phe Trp Ser Leu Ser Gly Ser Ser Arg				
	20	25	30	
gct act gtc gct act gga cgg tgc cgt agt cgt cgt ata gtg cgt cgt				144
Ala Thr Val Ala Thr Gly Arg Ser Arg Ser Arg Arg Ile Val Arg Arg				
	35	40	45	
gga cct cat gga gat gat agc tac gtg ctt ccg atc gtc gta gat aaa				192
Gly Pro His Gly Asp Asp Ser Tyr Val Leu Pro Ile Val Val Asp Lys				
	50	55	60	
tgg ttg ggc cgt tca ctg acc gtc atc ctc aag cac ggg cta cgg cgg				240
Trp Leu Gly Arg Ser Leu Thr Val Ile Leu Lys His Gly Leu Arg Arg				
	65	70	75	80
ctc gtc gag gac gat aag cac ccg ccc ctc ctc tgg gga tat gtg gct				288
Leu Val Glu Asp Asp Lys His Pro Pro Leu Leu Trp Gly Tyr Val Ala				
	85	90	95	
cca gtg tgg ggg ggc ccc agt gac cca ttt gtt gaa atg ata taa				333
Pro Val Trp Gly Gly Pro Ser Asp Pro Phe Val Glu Met Ile *				
	100	105	110	

<210> 38

<211> 110

<212> PRT

<213> Homo sapiens

<400> 38

Met Ser Val Val Glu Val Gln Gly Leu Val Cys Tyr Ala Arg Arg Pro				
1	5	10	15	
Leu Ile Leu Pro Leu Leu Leu Phe Trp Ser Leu Ser Gly Ser Ser Arg				
	20	25	30	
Ala Thr Val Ala Thr Gly Arg Ser Arg Ser Arg Arg Ile Val Arg Arg				
	35	40	45	
Gly Pro His Gly Asp Asp Ser Tyr Val Leu Pro Ile Val Val Asp Lys				
	50	55	60	
Trp Leu Gly Arg Ser Leu Thr Val Ile Leu Lys His Gly Leu Arg Arg				
	65	70	75	80

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<210> 39
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(441)
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<400> 39																
ctg	cag	agc	tat	aga	tcc	aac	tgc	cag	ctg	gac	aaa	ccc	aac	tca	tct	48
Leu	Gln	Ser	Tyr	Arg	Ser	Asn	Cys	Gln	Leu	Asp	Lys	Pro	Asn	Ser	Ser	
1			5			10			15							
cca	gcc	atg	gcc	cct	cct	gat	gga	gca	gcc	ctt	ctg	ctg	ctg	ctg	ctg	96
Pro	Ala	Met	Ala	Pro	Pro	Asp	Gly	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	
			20			25			30							
ctg	ttt	acg	gct	gct	tca	ata	aaa	act	gct	aac	tcc	att	ggc	tcg	ccc	144
Leu	Phe	Thr	Ala	Ala	Ser	Ile	Lys	Thr	Ala	Asn	Ser	Ile	Gly	Ser	Pro	
35						40			45							
tta	cct	tct	ttc	ttg	ggt	gaa	gcc	aca	aac	cct	cct	ggg	agg	cat	gta	192
Leu	Pro	Ser	Phe	Leu	Gly	Glu	Ala	Thr	Asn	Pro	Pro	Gly	Arg	His	Val	
50						55			60							
aag	cgg	tat	ggt	cac	ttt	gaa	gag	cag	ttg	ggt	cac	ttc	tta	aaa	agt	240
Lys	Arg	Tyr	Gly	His	Phe	Glu	Glu	Gln	Leu	Gly	His	Phe	Leu	Lys	Ser	
65			70			75			80							
gaa	acc	tac	tat	atg	acc	cag	tca	ttc	tgc	tcc	tat	gca	cct	cct	caa	288
Glu	Thr	Tyr	Tyr	Met	Thr	Gln	Ser	Phe	Cys	Ser	Tyr	Ala	Pro	Pro	Gln	
			85			90			95							
cag	caa	tgt	ggc	cag	ggt	gcc	cag	gat	gag	tgt	gag	aag	gag	ggc	tgc	336
Gln	Gln	Cys	Gly	Gln	Gly	Ala	Gln	Asp	Glu	Cys	Glu	Lys	Glu	Gly	Cys	
			100			105			110							

act tcc ctc gag ggg ctg gct gag ctc ctt ggt gct caa tgt cgt acc 432
Thr Ser Leu Glu Gly Leu Ala Glu Leu Leu Gly Ala Gln Cys Arg Thr
130 135 140

att tac tga 441
Ile Tyr *
145

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<210> 40
<211> 146
<212> PRT
<213> Homo sapiens
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[illegible]

<210>	41
<211>	441
<212>	DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(441)

<400> 41

atg ctg ttg ctg cag ctg ctg ctg ctg ctg ccg ccg ctg ctg ctc ctg	48
Met Leu Leu Leu Gln Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu	
1 5 10 15	
ctt ttt tca gtc tca ctc tgt tgc cca ggc tgg agt gaa gtg ggc atg	96
Leu Phe Ser Val Ser Leu Cys Cys Pro Gly Trp Ser Glu Val Gly Met	
20 25 30	
gaa gtc aaa cca ggt ctc cct tcc cac aac tcg ctg ccc cag ccc atg	144
Glu Val Lys Pro Gly Leu Pro Ser His Asn Ser Leu Pro Gln Pro Met	
35 40 45	
gca gat gga cat ccc cca agg gca tta caa cca tgg cac aag gac acc	192
Ala Asp Gly His Pro Pro Arg Ala Leu Gln Pro Trp His Lys Asp Thr	
50 55 60	
ctt ggt cca gag gga agt tgc aaa gtc tgg ttt gcc tgg aag gag ctc	240
Leu Gly Pro Glu Gly Ser Cys Lys Val Trp Phe Ala Trp Lys Glu Leu	
65 70 75 80	
ttc cag gtg gag gaa gcg gca gat aaa gaa act gaa gtt cag agt gtc	288
Phe Gln Val Glu Glu Ala Ala Asp Lys Glu Thr Glu Val Gln Ser Val	
85 90 95	
agc tta ccc aag gtc aca tct gaa aag cag cag aga cag gtt tca acc	336
Ser Leu Pro Lys Val Thr Ser Glu Lys Gln Gln Arg Gln Val Ser Thr	
100 105 110	
cag att ggg ctg act cca agc ccc atg ctg att ccc tgt ggc acc tgc	384
Gln Ile Gly Leu Thr Pro Ser Pro Met Leu Ile Pro Cys Gly Thr Cys	
115 120 125	
ctc tcg gct ggt aca gaa aac cag gga aag ctg tat ttg aat ctc aac	432
Leu Ser Ala Gly Thr Glu Asn Gln Gly Lys Leu Tyr Leu Asn Leu Asn	
130 135 140	

cca atc tga
Pro Ile *
145

441

<210> 42
<211> 146
<212> PRT
<213> Homo sapiens

<400> 42

Met Leu Leu Leu Gln Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu
1 5 10 15
Leu Phe Ser Val Ser Leu Cys Cys Pro Gly Trp Ser Glu Val Gly Met
20 25 30
Glu Val Lys Pro Gly Leu Pro Ser His Asn Ser Leu Pro Gln Pro Met
35 40 45
Ala Asp Gly His Pro Pro Arg Ala Leu Gln Pro Trp His Lys Asp Thr
50 55 60
Leu Gly Pro Glu Gly Ser Cys Lys Val Trp Phe Ala Trp Lys Glu Leu
65 70 75 80
Phe Gln Val Glu Glu Ala Ala Asp Lys Glu Thr Glu Val Gln Ser Val
85 90 95
Ser Leu Pro Lys Val Thr Ser Glu Lys Gln Gln Arg Gln Val Ser Thr
100 105 110
Gln Ile Gly Leu Thr Pro Ser Pro Met Leu Ile Pro Cys Gly Thr Cys
115 120 125
Leu Ser Ala Gly Thr Glu Asn Gln Gly Lys Leu Tyr Leu Asn Leu Asn
130 135 140
Pro Ile
145

<210> 43
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(203)

<400> 43

atg act ggc tgt ccg gcg tca tca aga cgc cga ggc ttc ggg ctc ttt

48

$\langle 220 \rangle$

$\langle 222 \rangle \quad (1) \dots (441)$

atg gcc ctg tct tgg ctg gcc ctg tcc ccc ggg tta cag ggc cag aac 48
Met Ala Leu Ser Trp Leu Ala Leu Ser Pro Gly Leu Gln Gly Gln Asn
1 5 10 15

ctg ctg gaa gca ggg cgc agg acc agc cag atc cca cca ggc tcc ctg 96
Leu Leu Glu Ala Gly Arg Arg Thr Ser Gln Ile Pro Pro Gly Ser Leu
20 25 30

agg gac tat aca gtg cct ctg tgc cgc ctg gag ccc agg ccc gcc ttc 144
Arg Asp Tyr Thr Val Pro Leu Cys Arg Leu Glu Pro Arg Pro Ala Phe
35 40 45

tcc gtg gcc gcc ctg gcc ttg agg gcc acc agc ctg gct gcg cag ggc 192
Ser Val Ala Ala Leu Ala Leu Arg Ala Thr Ser Leu Ala Ala Gln Gly
50 55 60

tat gaa gaa ggc atg gaa gac aag gat aac tca ggg aac aga gaa gat 240
Tyr Glu Glu Gly Met Glu Asp Lys Asp Asn Ser Gly Asn Arg Glu Asp
65 70 75 80

ggc agc aca gat agt gtc act tgg ggt ttt gag aaa ggc gat aga tat 288
Gly Ser Thr Asp Ser Val Thr Trp Gly Phe Glu Lys Gly Asp Arg Tyr
85 90 95

tgg ctg cca ctc aga tca tgt ggg ata atg atg cta gaa cag gtt tcc 336
Trp Leu Pro Leu Arg Ser Cys Gly Ile Met Met Leu Glu Gln Val Ser
100 105 110

```
acc ttc att cat atg cag gag gac ttt gac cag gtt ctc aca gta aat      384
Thr Phe Ile His Met Gln Glu Asp Phe Asp Gln Val Leu Thr Val Asn
      115              120              125
```

atg gaa gaa aaa tct ccc cta gct tct agc agg gga aaa gaa aag gag 432
Met Glu Glu Lys Ser Pro Leu Ala Ser Ser Arg Gly Lys Glu Lys Glu
130 135 140

acc act tag 441
Thr Thr *
145

<210> 46
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Ala Leu Ser Trp Leu Ala Leu Ser Pro Gly Leu Gln Gly Gln Asn
 1 5 10 15
 Leu Leu Glu Ala Gly Arg Arg Thr Ser Gln Ile Pro Pro Gly Ser Leu
 20 25 30
 Arg Asp Tyr Thr Val Pro Leu Cys Arg Leu Glu Pro Arg Pro Ala Phe
 35 40 45
 Ser Val Ala Ala Leu Ala Leu Arg Ala Thr Ser Leu Ala Ala Gln Gly
 50 55 60
 Tyr Glu Glu Gly Met Glu Asp Lys Asp Asn Ser Gly Asn Arg Glu Asp
 65 70 75 80
 Gly Ser Thr Asp Ser Val Thr Trp Gly Phe Glu Lys Gly Asp Arg Tyr
 85 90 95
 Trp Leu Pro Leu Arg Ser Cys Gly Ile Met Met Leu Glu Gln Val Ser
 100 105 110
 Thr Phe Ile His Met Gln Glu Asp Phe Asp Gln Val Leu Thr Val Asn
 115 120 125
 Met Glu Glu Lys Ser Pro Leu Ala Ser Ser Arg Gly Lys Glu Lys Glu
 130 135 140
 Thr Thr
 145

<210> 47
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(384)

<400> 47

atg gta aag ctg ctg ctc tcc ctg ctg tcc aca act ggg gcc tgg agc
 Met Val Lys Leu Leu Leu Ser Leu Leu Ser Thr Thr Gly Ala Trp Ser
 1 5 10 15

Met Val Lys Leu Leu Leu Ser Leu Leu Ser Thr Thr Gly Ala Trp Ser
1 5 10 15
Trp Gly His Ile Leu Gln Pro Glu Gly Ser Trp Glu Leu Trp Leu Pro
20 25 30
Gly Ser Thr Val Ala Pro Thr Asp Leu Gln Trp Val Leu His Pro Gly
35 40 45
Leu Leu Ser Glu Thr Asn Thr Leu Pro Ser Phe Leu Leu Gly Thr Val
50 55 60

Thr Thr Arg Thr Tyr Cys Ala Ser Gly Thr Val Gln Arg Leu Asp Ile
 65 70 75 80
 Ser Leu Leu Gln Pro Trp Gly Tyr Glu Lys Pro Cys Pro Ile Leu Ala
 85 90 95
 Glu Gly Ala Glu Val Gly Arg Arg Val Gly Thr Thr Glu Ser Arg Glu
 100 105 110
 Leu Asn Thr His Lys Glu Ser Lys Ile Cys Phe Tyr Ser Glu Ser
 115 120 125

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<210> 49
<211> 1110
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(1110)

<400> 49																
atg	cca	ccc	atg	ctg	tgg	ctg	ctg	ctc	cac	ttt	gct	gcc	ccg	gca	ctg	48
Met	Pro	Pro	Met	Leu	Trp	Leu	Leu	Leu	His	Phe	Ala	Ala	Pro	Ala	Leu	
1			5			10			15							
<400> 96																
ggg	ttc	tac	ttt	tcc	atc	agc	tgc	ccc	agt	ggg	aag	cag	tgc	caa	cag	96
Gly	Phe	Tyr	Phe	Ser	Ile	Ser	Cys	Pro	Ser	Gly	Lys	Gln	Cys	Gln	Gln	
20			25			30										
<400> 144																
gcc	cta	ctc	tca	ggc	aat	gat	att	ctc	ctg	tat	tgc	aac	tcc	tcg	ggg	144
Ala	Leu	Leu	Ser	Gly	Asn	Asp	Ile	Leu	Leu	Tyr	Cys	Asn	Ser	Ser	Gly	
35			40			45										
<400> 192																
gcg	cac	tgg	tac	tat	tta	ttc	aca	caa	ggc	aag	aag	ggc	agg	ctc	acc	192
Ala	His	Trp	Tyr	Tyr	Leu	Phe	Thr	Gln	Gly	Lys	Lys	Gly	Arg	Leu	Thr	
50			55			60										
<400> 240																
agc	ctc	acc	aat	att	tcc	aat	atg	gaa	ata	atg	ccc	gag	ggc	agc	ctt	240
Ser	Leu	Thr	Asn	Ile	Ser	Asn	Met	Glu	Ile	Met	Pro	Glu	Gly	Ser	Leu	
65			70			75			80							
<400> 288																
ctc	att	aaa	gat	cca	ttg	ccc	tcc	cag	acg	ggc	ctc	tac	cac	tgc	tgg	288
Leu	Ile	Lys	Asp	Pro	Leu	Pro	Ser	Gln	Thr	Gly	Leu	Tyr	His	Cys	Trp	
85			90			95										

aac aag aat ggc cgc caa gtg gtg cag tat gaa att gac ttt cag gat	336
Asn Lys Asn Gly Arg Gln Val Val Gln Tyr Glu Ile Asp Phe Gln Asp	
100 105 110	
gtc acc acc ctg cat ata aca cac aag gac ctg ggt cag agg ccc ctg	384
Val Thr Thr Leu His Ile Thr His Lys Asp Leu Gly Gln Arg Pro Leu	
115 120 125	
cag aac gag acc ctg cat ttg ggc agc aaa cag ctc att ttt acc tgg	432
Gln Asn Glu Thr Leu His Leu Gly Ser Lys Gln Leu Ile Phe Thr Trp	
130 135 140	
tgg gag ccc tgg cag gac tgc aac cgc tgt gag gag ccg ggc gag tgt	480
Trp Glu Pro Trp Gln Asp Cys Asn Arg Cys Glu Glu Pro Gly Glu Cys	
145 150 155 160	
aaa cgc ctg ggg tac cgc tac att gag gag cct ctg gag gaa gcc atg	528
Lys Arg Leu Gly Tyr Arg Tyr Ile Glu Glu Pro Leu Glu Glu Ala Met	
165 170 175	
ccc tgc tgg ctc tat ctg gga gag gtg ctg gtg tgg tct agc cgc ttg	576
Pro Cys Trp Leu Tyr Leu Gly Glu Val Leu Val Trp Ser Ser Arg Leu	
180 185 190	
cgg cct gag ctg cag gtg gaa gcc tgc cac gtc cag tgc acc aat aac	624
Arg Pro Glu Leu Gln Val Glu Ala Cys His Val Gln Cys Thr Asn Asn	
195 200 205	
aca cag tta agg gtg gat tac gtc att ttt gac aac ttc agg ctc gat	672
Thr Gln Leu Arg Val Asp Tyr Val Ile Phe Asp Asn Phe Arg Leu Asp	
210 215 220	
gag aag aca gaa ttt gtg tgg ctc gac tgt ccc tta gga tcc atg tac	720
Glu Lys Thr Glu Phe Val Trp Leu Asp Cys Pro Leu Gly Ser Met Tyr	
225 230 235 240	
agg ccc gtc aac tgg cgt gcc aac gac acc ccc ctg acg tgg gag agc	768
Arg Pro Val Asn Trp Arg Ala Asn Asp Thr Pro Leu Thr Trp Glu Ser	
245 250 255	
cag ctc tcc ggc cag gac ttc acc acc ttt ctg gac ccc tcc acc ggc	816
Gln Leu Ser Gly Gln Asp Phe Thr Thr Phe Leu Asp Pro Ser Thr Gly	
260 265 270	

ggc agg cag ctg cag gtt ttc cag ccg gcc gtc tac aag tgc ttc gtg 864
 Gly Arg Gln Leu Gln Val Phe Gln Pro Ala Val Tyr Lys Cys Phe Val
 275 280 285

cag cag gag ctc gtg gcc cag ttc aaa ccc gcc gcc agt ctg gag acg 912
 Gln Gln Glu Leu Val Ala Gln Phe Lys Pro Ala Ala Ser Leu Glu Thr
 290 295 300

ctg gag gct cag tgg aga gag aac gat gcc cag tgg cgg gag gca agg 960
 Leu Glu Ala Gln Trp Arg Glu Asn Asp Ala Gln Trp Arg Glu Ala Arg
 305 310 315 320

aag gcc ctg cgg ggc agg gcg gac tcc gtg ctc aag ggg ctg aag ctg 1008
 Lys Ala Leu Arg Gly Arg Ala Asp Ser Val Leu Lys Gly Leu Lys Leu
 325 330 335

gtg ctg ctc gtg gtc acc gtc ctg gcc ctg ctg ggg gcg ctg ctc aag 1056
 Val Leu Leu Val Val Thr Val Leu Ala Leu Leu Gly Ala Leu Leu Lys
 340 345 350

tgc atc cac cct tcc ccg ggc agg aga agc aca cag gtg ctg gtg gtg 1104
 Cys Ile His Pro Ser Pro Gly Arg Arg Ser Thr Gln Val Leu Val Val
 355 360 365

aaa taa 1110
 Lys *

<210> 50

<211> 369

<212> PRT

<213> Homo sapiens

<400> 50

Met Pro Pro Met Leu Trp Leu Leu Leu His Phe Ala Ala Pro Ala Leu
 1 5 10 15
 Gly Phe Tyr Phe Ser Ile Ser Cys Pro Ser Gly Lys Gln Cys Gln Gln
 20 25 30
 Ala Leu Leu Ser Gly Asn Asp Ile Leu Leu Tyr Cys Asn Ser Ser Gly
 35 40 45
 Ala His Trp Tyr Tyr Leu Phe Thr Gln Gly Lys Lys Gly Arg Leu Thr

50 55 60
 Ser Leu Thr Asn Ile Ser Asn Met Glu Ile Met Pro Glu Gly Ser Leu
 65 70 75 80
 Leu Ile Lys Asp Pro Leu Pro Ser Gln Thr Gly Leu Tyr His Cys Trp
 85 90 95
 Asn Lys Asn Gly Arg Gln Val Val Gln Tyr Glu Ile Asp Phe Gln Asp
 100 105 110
 Val Thr Thr Leu His Ile Thr His Lys Asp Leu Gly Gln Arg Pro Leu
 115 120 125
 Gln Asn Glu Thr Leu His Leu Gly Ser Lys Gln Leu Ile Phe Thr Trp
 130 135 140
 Trp Glu Pro Trp Gln Asp Cys Asn Arg Cys Glu Glu Pro Gly Glu Cys
 145 150 155 160
 Lys Arg Leu Gly Tyr Arg Tyr Ile Glu Glu Pro Leu Glu Glu Ala Met
 165 170 175
 Pro Cys Trp Leu Tyr Leu Gly Glu Val Leu Val Trp Ser Ser Arg Leu
 180 185 190
 Arg Pro Glu Leu Gln Val Glu Ala Cys His Val Gln Cys Thr Asn Asn
 195 200 205
 Thr Gln Leu Arg Val Asp Tyr Val Ile Phe Asp Asn Phe Arg Leu Asp
 210 215 220
 Glu Lys Thr Glu Phe Val Trp Leu Asp Cys Pro Leu Gly Ser Met Tyr
 225 230 235 240
 Arg Pro Val Asn Trp Arg Ala Asn Asp Thr Pro Leu Thr Trp Glu Ser
 245 250 255
 Gln Leu Ser Gly Gln Asp Phe Thr Thr Phe Leu Asp Pro Ser Thr Gly
 260 265 270
 Gly Arg Gln Leu Gln Val Phe Gln Pro Ala Val Tyr Lys Cys Phe Val
 275 280 285
 Gln Gln Glu Leu Val Ala Gln Phe Lys Pro Ala Ala Ser Leu Glu Thr
 290 295 300
 Leu Glu Ala Gln Trp Arg Glu Asn Asp Ala Gln Trp Arg Glu Ala Arg
 305 310 315 320
 Lys Ala Leu Arg Gly Arg Ala Asp Ser Val Leu Lys Gly Leu Lys Leu
 325 330 335
 Val Leu Leu Val Val Thr Val Leu Ala Leu Leu Gly Ala Leu Leu Lys
 340 345 350
 Cys Ile His Pro Ser Pro Gly Arg Arg Ser Thr Gln Val Leu Val Val
 355 360 365
 Lys

<211> 759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(759)

<400> 51

atg gca gcc ccc gcc ctg ctg ctc cta gca ctg ctg ctg ccc gtg ggg	48
Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly	
1 5 10 15	

gcc tgg ccc ggg ctg ccc agg agg ccc tgt gtg cac tgc tgc cgc ccg	96
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
20 25 30	

gcc tgg ccc cct gga ccc tat gcc cgg gtg agt gac agg gac ctg tgg	144
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
35 40 45	

agg ggg gac ctg tgg agg ggg ctg cct cga gta cgg ccc act ata gac	192
Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asp	
50 55 60	

atc gaa atc ctc aaa ggt gag aag ggt gag gcc ggc gtc cga ggt cgg	240
Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg	
65 70 75 80	

gcc ggc agg agc ggg aaa gag ggg ccg cca ggc gcc cgg ggc ctg cag	288
Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln	
85 90 95	

ggc cgc aga ggc cag aag ggg cag gtg ggg ccg ccg ggc gcc gcg tgc	336
Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys	
100 105 110	

cga cgt gcc tac gcc gcc ttc tcc gtg ggc cgg cgc gag ggc ctg cac	384
Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His	
115 120 125	

agc tcc gac cac ttc cag gcg gtg ccc ttc gac acg gag ctg gtg aac	432
Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn	

130	135	140	
ctg gac ggc gcc ttc gac ctg gcc gcg ggc cgc ttc ctc tgc acg gtg			480
Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val			
145	150	155	160
ccc ggc gtc tac ttc ctc agc ctc aac gtg cac acc tgg aac tac aag			528
Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys			
	165	170	175
gag acc tac ctg cac atc atg ctg aac cgg cgg ccc gcg gcc gtg ctc			576
Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu			
	180	185	190
tac gcg cag ccc agc gag cgc agc gtc atg cag gcc cag agc ctg atg			624
Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met			
	195	200	205
ctg ctg ctg gcg gcg ggc gac gcc gtc tgg gtg cgc atg ttc cag cgc			672
Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg			
	210	215	220
gac cgg gac aac gcc atc tac ggc gag cac gga gac ctc tac atc acc			720
Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr			
225	230	235	240
ttc agc ggc cac ctg gtc aag ccg gcc gcc gag ctg tag			759
Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu *			
	245	250	

<210> 52

<211> 252

<212> PRT

<213> Homo sapiens

<400> 52

Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly	
1	5
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
	20
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
	35
	40
	45

F03390.122660

Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asp
 50 55 60
 Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg
 65 70 75 80
 Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln
 85 90 95
 Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys
 100 105 110
 Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His
 115 120 125
 Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn
 130 135 140
 Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val
 145 150 155 160
 Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys
 165 170 175
 Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu
 180 185 190
 Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met
 195 200 205
 Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg
 210 215 220
 Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr
 225 230 235 240
 Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu
 245 250

<210> 53
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(293)

<400> 53

atg cag gcc ccc tcg ctc ctc agc gtg gtg gcc gtc tgg ctg acc tgg 48
 Met Gln Ala Pro Ser Leu Leu Ser Val Val Ala Val Trp Leu Thr Trp
 1 5 10 15

gcc aat ggg gcc atc aac cct gtc atc tac gcc atc cgc aat ccc aac 96
 Ala Asn Gly Ala Ile Asn Pro Val Ile Tyr Ala Ile Arg Asn Pro Asn

20	25	30	
att tcg atg ctc cta ggg cgc aac cgc gag gag ggc tac cgg act agg			144
Ile Ser Met Leu Leu Gly Arg Asn Arg Glu Glu Gly Tyr Arg Thr Arg			
35	40	45	
aat gtg gac gct ttc ctg ccc agc cag ggc ccg ggt ctg caa gcc aga			192
Asn Val Asp Ala Phe Leu Pro Ser Gln Gly Pro Gly Leu Gln Ala Arg			
50	55	60	
agc cgc agt cgc ctt cga aac cgc tat gcc aac cgg ctg ggg gcc tgc			240
Ser Arg Ser Arg Leu Arg Asn Arg Tyr Ala Asn Arg Leu Gly Ala Cys			
65	70	75	80
aac agg atg tcc tct tcc aac ccg gcc agc gga gtg gca ggg gac gtg			288
Asn Arg Met Ser Ser Ser Asn Pro Ala Ser Gly Val Ala Gly Asp Val			
85	90	95	
gcc at			293
Ala			

<210> 54
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 54

Met Gln Ala Pro Ser Leu Leu Ser Val Val Ala Val Trp Leu Thr Trp			
1	5	10	15
Ala Asn Gly Ala Ile Asn Pro Val Ile Tyr Ala Ile Arg Asn Pro Asn			
20	25	30	
Ile Ser Met Leu Leu Gly Arg Asn Arg Glu Glu Gly Tyr Arg Thr Arg			
35	40	45	
Asn Val Asp Ala Phe Leu Pro Ser Gln Gly Pro Gly Leu Gln Ala Arg			
50	55	60	
Ser Arg Ser Arg Leu Arg Asn Arg Tyr Ala Asn Arg Leu Gly Ala Cys			
65	70	75	80
Asn Arg Met Ser Ser Ser Asn Pro Ala Ser Gly Val Ala Gly Asp Val			
85	90	95	
Ala			

<220>
<221> CDS
<222> (1)...(258)

<210> 56
<211> 85
<212> PRT
<213> Homo sapiens

<400> 56
Met Ser Pro Pro Pro Pro Leu Leu Leu Leu Leu Leu Ser Leu Ala

1 5 10 15
 Leu Leu Gly Ala Arg Ala Arg Ala Glu Pro Ala Gly Ser Ala Val Pro
 20 25 30
 Ala Gln Ser Arg Pro Cys Val Asp Cys His Ala Phe Glu Phe Met Gln
 35 40 45
 Arg Ala Leu Gln Asp Leu Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg
 50 55 60
 Thr Glu Thr Leu Leu Leu Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys
 65 70 75 80
 Trp Pro Ala Gly His
 85

<210> 57
 <211> 570
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(570)

<400> 57

atg gag gaa caa gcc aca cag ggg gtt cca aag tct cca ggg gat gct 48
 Met Glu Glu Gln Ala Thr Gln Gly Val Pro Lys Ser Pro Gly Asp Ala
 1 5 10 15

gag gaa gcc ttc ctt gcc ctg tcc tgg gtc ttg gcc agc ggt ggg ctc 96
 Glu Glu Ala Phe Leu Ala Leu Ser Trp Val Leu Ala Ser Gly Gly Leu
 20 25 30

ccc agg gac ctc acc agg acg gca ttt tgc gag agc cga agc cgg aag 144
 Pro Arg Asp Leu Thr Arg Thr Ala Phe Cys Glu Ser Arg Ser Arg Lys
 35 40 45

cgg cct cgg ggt gcg ctg cac cgc ctc ttc cgg ggc ctc tct agg ccg 192
 Arg Pro Arg Gly Ala Leu His Arg Leu Phe Arg Gly Leu Ser Arg Pro
 50 55 60

gag cgc ggg att tcg gtg gcc ggg aga ggc cgg aac ggc ttc gcg ggg 240
 Glu Arg Gly Ile Ser Val Ala Gly Arg Gly Arg Asn Gly Phe Ala Gly
 65 70 75 80

cag cgg cgc ctc ctg gcg ggc ctg ggg tca ggc agt ccg tgg ggg gtc 288

Gln Arg Arg Leu Leu Ala Gly Leu Gly Ser Gly Ser Pro Trp Gly Val
 85 90 95

tgg ctg gct ccc tgc agt aca cac ctg cgc cga tgc cca gcg ttg agg 336
 Trp Leu Ala Pro Cys Ser Thr His Leu Arg Arg Cys Pro Ala Leu Arg
 100 105 110

ccc tac cca tcc cgg ggg acc ttt ccc ctc ccg cct ccc gcc ctt ctg 384
 Pro Tyr Pro Ser Arg Gly Thr Phe Pro Leu Pro Pro Pro Ala Leu Leu
 115 120 125

tcg gct ttc ttc cca cgg atc tgc cag gaa gcc ttc cag gac tgt cct 432
 Ser Ala Phe Phe Pro Arg Ile Cys Gln Glu Ala Phe Gln Asp Cys Pro
 130 135 140

gga gca tca agg ctc gac cgc acg gcc atg ggt acc gac cat ccc agc 480
 Gly Ala Ser Arg Leu Asp Arg Thr Ala Met Gly Thr Asp His Pro Ser
 145 150 155 160

cac acg gct ggg caa cgt gtg gtg ggt cac cgc gca gcc aga ctc cgg 528
 His Thr Ala Gly Gln Arg Val Val Gly His Arg Ala Ala Arg Leu Arg
 165 170 175

ctg gtg acc gcc agg ggt cag cag agg cct cct ttt gca tag 570
 Leu Val Thr Ala Arg Gly Gln Gln Arg Pro Pro Phe Ala *
 180 185

<210> 58
 <211> 189
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Glu Glu Gln Ala Thr Gln Gly Val Pro Lys Ser Pro Gly Asp Ala
 1 5 10 15
 Glu Glu Ala Phe Leu Ala Leu Ser Trp Val Leu Ala Ser Gly Gly Leu
 20 25 30
 Pro Arg Asp Leu Thr Arg Thr Ala Phe Cys Glu Ser Arg Ser Arg Lys
 35 40 45
 Arg Pro Arg Gly Ala Leu His Arg Leu Phe Arg Gly Leu Ser Arg Pro
 50 55 60
 Glu Arg Gly Ile Ser Val Ala Gly Arg Gly Arg Asn Gly Phe Ala Gly

Ser Ser Ser Ala Met Gly Thr Asp Glu Thr Leu Lys Ala Ser Gly Leu
 65 70 75 80
 gcg tca acc gaa gag aca ccg gcc aag cac agt gac cgc aac cgg ctg 288
 Ala Ser Thr Glu Glu Thr Pro Ala Lys His Ser Asp Arg Asn Arg Leu
 85 90 95
 gaa caa acc cca cgg gac cca gag tgg gac cag gcc tgg ggg cgc aag 336
 Glu Gln Thr Pro Arg Asp Pro Glu Trp Asp Gln Ala Trp Gly Arg Lys
 100 105 110
 gag gcc cgg ctg cca tcc gtc gca tgc gca aag gag ggg ctc acc caa 384
 Glu Ala Arg Leu Pro Ser Val Ala Cys Ala Lys Glu Gly Leu Thr Gln
 115 120 125
 caa acg ata tgc agc gcc gcg gtt tct gcg ccg ctg gtc ccc acg gtg 432
 Gln Thr Ile Cys Ser Ala Ala Val Ser Ala Pro Leu Val Pro Thr Val
 130 135 140
 gag tca cac acg cag tcc gtt gac cct gta aag gga aaa aga agg tcc 480
 Glu Ser His Thr Gln Ser Val Asp Pro Val Lys Gly Lys Arg Arg Ser
 145 150 155 160
 caa ata gca tca gaa taa 498
 Gln Ile Ala Ser Glu *
 165

<210> 60
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Arg Lys Ile Leu Phe Leu Asn Leu Trp Ile Ser Leu Val Lys Ala
 1 5 10 15
 Ser Thr Tyr Gln Gly Glu Gln Glu Ala Arg Gly Thr Asn Asn Thr Glu
 20 25 30
 Phe Asp Ala Lys Lys Gly Asp Phe Ser Ser Gly Cys Ile Lys Thr Gly
 35 40 45
 Gly Arg Phe Asn Ala Trp Ile Asn Gly Ser Val Tyr Leu His Arg Arg
 50 55 60
 Ser Ser Ser Ala Met Gly Thr Asp Glu Thr Leu Lys Ala Ser Gly Leu

TGGGG'ACGGGG

65 70 75 80
 Ala Ser Thr Glu Glu Thr Pro Ala Lys His Ser Asp Arg Asn Arg Leu
 85 90 95
 Glu Gln Thr Pro Arg Asp Pro Glu Trp Asp Gln Ala Trp Gly Arg Lys
 100 105 110
 Glu Ala Arg Leu Pro Ser Val Ala Cys Ala Lys Glu Gly Leu Thr Gln
 115 120 125
 Gln Thr Ile Cys Ser Ala Ala Val Ser Ala Pro Leu Val Pro Thr Val
 130 135 140
 Glu Ser His Thr Gln Ser Val Asp Pro Val Lys Gly Lys Arg Arg Ser
 145 150 155 160
 Gln Ile Ala Ser Glu
 165

<210> 61
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(462)

<400> 61

atg cac ctg cgg ctg cta cca cta ctg ctt ctg cta atg ctg tcg tta 48
 Met His Leu Arg Leu Leu Pro Leu Leu Leu Leu Leu Met Leu Ser Leu
 1 5 10 15

aaa ctg atg gct acc acg cgt ggt cga tta tgt gct acg tct tgt gca 96
 Lys Leu Met Ala Thr Thr Arg Gly Arg Leu Cys Ala Thr Ser Cys Ala
 20 25 30

aga ctc caa gtt ctt cag tgt cga act ctt gga ctt aca cca gtg gtt 144
 Arg Leu Gln Val Leu Gln Cys Arg Thr Leu Gly Leu Thr Pro Val Val
 35 40 45

tgc cag cgg ctc tcg agc ctt ctg cta cag act gaa ggc tac gct ctc 192
 Cys Gln Arg Leu Ser Ser Leu Leu Gln Thr Glu Gly Tyr Ala Leu
 50 55 60

ggc ttc cct act ttt agg gct ttg gga ctt gaa ctg gct tcc ttg ctc 240
 Gly Phe Pro Thr Phe Arg Ala Leu Gly Leu Glu Leu Ala Ser Leu Leu
 65 70 75 80

<400> 62															
Met	His	Leu	Arg	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Met	Leu	Ser	Leu
1				5					10					15	
Lys	Leu	Met	Ala	Thr	Thr	Arg	Gly	Arg	Leu	Cys	Ala	Thr	Ser	Cys	Ala
			20					25					30		
Arg	Leu	Gln	Val	Leu	Gln	Cys	Arg	Thr	Leu	Gly	Leu	Thr	Pro	Val	Val
		35					40					45			
Cys	Gln	Arg	Leu	Ser	Ser	Leu	Leu	Leu	Gln	Thr	Glu	Gly	Tyr	Ala	Leu
	50					55					60				
Gly	Phe	Pro	Thr	Phe	Arg	Ala	Leu	Gly	Leu	Glu	Leu	Ala	Ser	Leu	Leu
65					70					75					80
Leu	Ser	Leu	Gln	Met	Ala	Tyr	Cys	Gly	Thr	Leu	Pro	Cys	Asp	His	Asn
				85					90					95	
Ala	Thr	Leu	Ser	Pro	Ala	Gly	Lys	Pro	Glu	Gln	Ile	Lys	Met	Ala	Ser
			100					105					110		
Ala	Pro	Gly	Gly	Asn	Gly	Asn	Phe	Gln	Arg	Asp	Arg	Lys	Lys	Met	Ile

115 120 125
 Gln Asn Leu Lys Ala Ile Ser Asp His Ile Ile Pro Thr Ala Tyr Glu
 130 135 140
 Glu Ile Asp Ala Gln Glu Ile Asn Val
 145 150

<210> 63
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(315)

<400> 63
 atg aag gtt gga gga ctc agc aag aca gct ttt tct tct acc ttc ttc 48
 Met Lys Val Gly Gly Leu Ser Lys Thr Ala Phe Ser Ser Thr Phe Phe
 1 5 10 15
 tcc ctg ctt ttt cca gcc tca ctg gca gct gat tgg atg gtg ccc acc 96
 Ser Leu Leu Phe Pro Ala Ser Leu Ala Ala Asp Trp Met Val Pro Thr
 20 25 30
 aca ttg tgg aca tta gaa cta aag ttt ctt ggg cct tta gac ttg agg 144
 Thr Leu Trp Thr Leu Glu Leu Lys Phe Leu Gly Pro Leu Asp Leu Arg
 35 40 45
 gct tac atc agt ggc ccc caa ttt ctc aaa ctt tca act tca aat aaa 192
 Ala Tyr Ile Ser Gly Pro Gln Phe Leu Lys Leu Ser Thr Ser Asn Lys
 50 55 60
 gtt aca tcc tca gat ccc cca ggt tct tct ttg gac tca gac tgg att 240
 Val Thr Ser Ser Asp Pro Pro Gly Ser Ser Leu Asp Ser Asp Trp Ile
 65 70 75 80
 aca tca aaa gct ttc ctg gtt ctt cag ttt gaa gac agc atg ttg tgg 288
 Thr Ser Lys Ala Phe Leu Val Leu Gln Phe Glu Asp Ser Met Leu Trp
 85 90 95
 gac ttc tca acc tct ata att gtg tga 315
 Asp Phe Ser Thr Ser Ile Ile Val *
 100

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<210> 64
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Lys Val Gly Gly Leu Ser Lys Thr Ala Phe Ser Ser Thr Phe Phe
 1 5 10 15
 Ser Leu Leu Phe Pro Ala Ser Leu Ala Ala Asp Trp Met Val Pro Thr
 20 25 30
 Thr Leu Trp Thr Leu Glu Leu Lys Phe Leu Gly Pro Leu Asp Leu Arg
 35 40 45
 Ala Tyr Ile Ser Gly Pro Gln Phe Leu Lys Leu Ser Thr Ser Asn Lys
 50 55 60
 Val Thr Ser Ser Asp Pro Pro Gly Ser Ser Leu Asp Ser Asp Trp Ile
 65 70 75 80
 Thr Ser Lys Ala Phe Leu Val Leu Gln Phe Glu Asp Ser Met Leu Trp
 85 90 95
 Asp Phe Ser Thr Ser Ile Ile Val
 100

<210> 65
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(339)

<400> 65
 atg tgg gat gaa tca agt aca acc aca tgt gtt cca aag gtc aat gag 48
 Met Trp Asp Glu Ser Ser Thr Thr Thr Cys Val Pro Lys Val Asn Glu
 1 5 10 15
 agg ctc ttc gtg ctt tta gca tta att ttg cct cca ttg aca tca gag 96
 Arg Leu Phe Val Leu Leu Ala Leu Ile Leu Pro Pro Leu Thr Ser Glu
 20 25 30
 att ctg gat aac aac cgc ctc aga caa ata ttt gta gtg ttt ggc cct 144
 Ile Leu Asp Asn Asn Arg Leu Arg Gln Ile Phe Val Val Phe Gly Pro

35	40	45	
cac aat ctt ctg caa gca gtt ggc cag aag aaa cac ata aaa cac aga			192
His Asn Leu Leu Gln Ala Val Gly Gln Lys Lys His Ile Lys His Arg			
50	55	60	
aca cag acg tat ctg gtc ttt tca gaa aca gca aat aga gag cca ctg			240
Thr Gln Thr Tyr Leu Val Phe Ser Glu Thr Ala Asn Arg Glu Pro Leu			
65	70	75	80
aaa act ggc tcc ctt ggg gct ctg caa gaa aca gct agc acc tct ggc			288
Lys Thr Gly Ser Leu Gly Ala Leu Gln Glu Thr Ala Ser Thr Ser Gly			
	85	90	95
gat gga ggc cag cca cac ctc act acc ttg aaa agt agg gta act cag			336
Asp Gly Gly Gln Pro His Leu Thr Thr Leu Lys Ser Arg Val Thr Gln			
	100	105	110
tag			339
*			

<210> 66
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 66

Met Trp Asp Glu Ser Ser Thr Thr Thr Cys Val Pro Lys Val Asn Glu			
1	5	10	15
Arg Leu Phe Val Leu Leu Ala Leu Ile Leu Pro Pro Leu Thr Ser Glu			
	20	25	30
Ile Leu Asp Asn Asn Arg Leu Arg Gln Ile Phe Val Val Phe Gly Pro			
	35	40	45
His Asn Leu Leu Gln Ala Val Gly Gln Lys Lys His Ile Lys His Arg			
	50	55	60
Thr Gln Thr Tyr Leu Val Phe Ser Glu Thr Ala Asn Arg Glu Pro Leu			
65	70	75	80
Lys Thr Gly Ser Leu Gly Ala Leu Gln Glu Thr Ala Ser Thr Ser Gly			
	85	90	95
Asp Gly Gly Gln Pro His Leu Thr Thr Leu Lys Ser Arg Val Thr Gln			
	100	105	110

<210> 67
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(264)

<400> 67

atg gct gtc tta gta ctt cgc ctg aca gtt gtc ctg gga ctg ctt gtc 48
 Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
 1 5 10 15

tta ttc ctg acc tgc tat gca gac gac aaa cca gac aag cca gac gac 96
 Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
 20 25 30

aag cca gac gac tcg ggc aaa gac cca aag cca gac ttc ccc aaa ttc 144
 Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
 35 40 45

cta agc ctc ctg ggc aca gag atc att gag aat gca gtc gag ttc atc 192
 Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile
 50 55 60

ctc cgc tcc atg tcc agg agc aca gga ttt atg gaa ttt gat gat aat 240
 Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn
 65 70 75 80

gaa gga aaa cat tca tca aag tga 264
 Glu Gly Lys His Ser Ser Lys *
 85

<210> 68
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 68

Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val

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<210> 69
<211> 357
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(357)

<400> 69																
atg	ggc	tca	aag	aag	gta	gaa	ggg	ttg	ggt	ccg	gac	gaa	ctg	ctg	ctg	48
Met	Gly	Ser	Lys	Lys	Val	Glu	Gly	Leu	Gly	Pro	Asp	Glu	Leu	Leu	Leu	
1			5			10			15							
tta	ctg	ttg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	96
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
			20			25			30							
tcc	agc	agg	gca	gaa	gac	tgc	agt	ggc	cgg	gtg	tcc	agt	gtt	gtt	ggg	144
Ser	Ser	Arg	Ala	Glu	Asp	Cys	Ser	Gly	Arg	Val	Ser	Ser	Val	Val	Gly	
35						40			45							
ccc	agt	ggg	agt	gaa	ctg	agc	tca	cca	ctg	tcc	ttg	cta	tca	gtc	cca	192
Pro	Ser	Gly	Ser	Glu	Leu	Ser	Ser	Pro	Leu	Ser	Leu	Leu	Ser	Val	Pro	
50						55			60							
ggg	ccg	cca	ctc	act	aca	atg	ata	gcc	ccc	aaa	ccc	agt	cat	aca	aga	240
Gly	Pro	Pro	Leu	Thr	Thr	Met	Ile	Ala	Pro	Lys	Pro	Ser	His	Thr	Arg	
65			70			75			80							
gga	agt	aac	ctg	aaa	tta	gtc	acc	aca	gga	gac	agg	gac	aca	aga	cct	288

<220>
<221> CDS
<222> (1)...(474)

<400> 71

atg aag gca gcc tgc tct tcc ctc tgc ttg tca ctg ttg gct tta gaa	48
Met Lys Ala Ala Cys Ser Ser Leu Cys Leu Ser Leu Leu Ala Leu Glu	
1 5 10 15	
gcc acc tgg gga tta gga gca gca ggt gac aag cac ttt gaa gat gcc	96
Ala Thr Trp Gly Leu Gly Ala Ala Gly Asp Lys His Phe Glu Asp Ala	
20 25 30	
ctc cca gtg tgc ggg ctg gct cct gat gtg cag tgt cgg cac ctc ggc	144
Leu Pro Val Ser Gly Leu Ala Pro Asp Val Gln Cys Arg His Leu Gly	
35 40 45	
act tgg ggc gac tgt tgt ggc tgt gct gat ttg ctc atg atg cgc cac	192
Thr Trp Gly Asp Cys Cys Gly Cys Ala Asp Leu Leu Met Met Arg His	
50 55 60	
gac ctg gac tcc agt tac ttg cac gtg gga tcc cct gct gtc gtc cgc	240
Asp Leu Asp Ser Ser Tyr Leu His Val Gly Ser Pro Ala Val Val Arg	
65 70 75 80	
aag tca ccg agg ggg tgt gga gga gcc ttg cct gac agc cgg agg gag	288
Lys Ser Pro Arg Gly Cys Gly Gly Ala Leu Pro Asp Ser Arg Arg Glu	
85 90 95	
ctg gag tct gaa atg tca gct gct ctt ttt aca gaa cgt tat gtc aca	336
Leu Glu Ser Glu Met Ser Ala Ala Leu Phe Thr Glu Arg Tyr Val Thr	
100 105 110	
ggc ctt caa ata aga gcg ccc aat ttc ggc tca aga cgc gca ctg agc	384
Gly Leu Gln Ile Arg Ala Pro Asn Phe Gly Ser Arg Arg Ala Leu Ser	
115 120 125	
aga gat atg gag ctg gcc ctg acc acg ctg tgg agc ccg tgc tgg tcc	432
Arg Asp Met Glu Leu Ala Leu Thr Thr Leu Trp Ser Pro Cys Trp Ser	
130 135 140	
ctc aag cct cca gcc acc tgc acg cgg ggc cag cca ggc cag	474
Leu Lys Pro Pro Ala Thr Cys Thr Arg Gly Gln Pro Gly Gln	
145 150 155	

<210> 72
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 72

Met Lys Ala Ala Cys Ser Ser Leu Cys Leu Ser Leu Leu Ala Leu Glu
 1 5 10 15
 Ala Thr Trp Gly Leu Gly Ala Ala Gly Asp Lys His Phe Glu Asp Ala
 20 25 30
 Leu Pro Val Ser Gly Leu Ala Pro Asp Val Gln Cys Arg His Leu Gly
 35 40 45
 Thr Trp Gly Asp Cys Cys Gly Cys Ala Asp Leu Leu Met Met Arg His
 50 55 60
 Asp Leu Asp Ser Ser Tyr Leu His Val Gly Ser Pro Ala Val Val Arg
 65 70 75 80
 Lys Ser Pro Arg Gly Cys Gly Gly Ala Leu Pro Asp Ser Arg Arg Glu
 85 90 95
 Leu Glu Ser Glu Met Ser Ala Ala Leu Phe Thr Glu Arg Tyr Val Thr
 100 105 110
 Gly Leu Gln Ile Arg Ala Pro Asn Phe Gly Ser Arg Arg Ala Leu Ser
 115 120 125
 Arg Asp Met Glu Leu Ala Leu Thr Thr Leu Trp Ser Pro Cys Trp Ser
 130 135 140
 Leu Lys Pro Pro Ala Thr Cys Thr Arg Gly Gln Pro Gly Gln
 145 150 155

<210> 73
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(411)

<400> 73

atg cgc ccg ctg ctg ctg acc aag agg gca tta ctt ctt cca tcc tca 48
 Met Arg Pro Leu Leu Leu Thr Lys Arg Ala Leu Leu Leu Pro Ser Ser
 1 5 10 15

cat ctg gct caa gcg gaa atg aag ctg gcc ttc ccc atg ttc aaa gtc 96
 His Leu Ala Gln Ala Glu Met Lys Leu Ala Phe Pro Met Phe Lys Val

	20	25	30	
cag gca tgc cag ccc gat tca cac tcg gct cag aga cct ctg acc caa				144
Gln Ala Cys Gln Pro Asp Ser His Ser Ala Gln Arg Pro Leu Thr Gln				
	35	40	45	
tta ccc ctg gtt cct ggt gag cct cgc tgc aag acg gaa gcc tgt cac				192
Leu Pro Leu Val Pro Gly Glu Pro Arg Cys Lys Thr Glu Ala Cys His				
	50	55	60	
ccc ggc ccc atc cct caa ggt gaa acg tgc tgg gcc ctg ctc ctc cac				240
Pro Gly Pro Ile Pro Gln Gly Glu Thr Cys Trp Ala Leu Leu Leu His				
	65	70	75	80
tgc tct gat cat caa gcc ttc atc cag ctc tgt gct ggg gcc acg gac				288
Cys Ser Asp His Gln Ala Phe Ile Gln Leu Cys Ala Gly Ala Thr Asp				
	85	90	95	
agc gtg tct gga ggc acc att gac gtg gga cag cat cat ggg acc gca				336
Ser Val Ser Gly Gly Thr Ile Asp Val Gly Gln His His Gly Thr Ala				
	100	105	110	
cat gca aga cat gcc cca aaa tgg tct cag aac cac act gct tct ggt				384
His Ala Arg His Ala Pro Lys Trp Ser Gln Asn His Thr Ala Ser Gly				
	115	120	125	
gca gcc cac agc ggt ctt ttc cta taa				411
Ala Ala His Ser Gly Leu Phe Leu *				
	130	135		

<210> 74

<211> 136

<212> PRT

<213> Homo sapiens

<400> 74

Met Arg Pro Leu Leu Thr Lys Arg Ala Leu Leu Leu Pro Ser Ser				
1	5	10	15	
His Leu Ala Gln Ala Glu Met Lys Leu Ala Phe Pro Met Phe Lys Val				
	20	25	30	
Gln Ala Cys Gln Pro Asp Ser His Ser Ala Gln Arg Pro Leu Thr Gln				
	35	40	45	

Leu Pro Leu Val Pro Gly Glu Pro Arg Cys Lys Thr Glu Ala Cys His
 50 55 60
 Pro Gly Pro Ile Pro Gln Gly Glu Thr Cys Trp Ala Leu Leu Leu His
 65 70 75 80
 Cys Ser Asp His Gln Ala Phe Ile Gln Leu Cys Ala Gly Ala Thr Asp
 85 90 95
 Ser Val Ser Gly Gly Thr Ile Asp Val Gly Gln His His Gly Thr Ala
 100 105 110
 His Ala Arg His Ala Pro Lys Trp Ser Gln Asn His Thr Ala Ser Gly
 115 120 125
 Ala Ala His Ser Gly Leu Phe Leu
 130 135

<210> 75

<211> 678

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(678)

<400> 75

atg tac ttg gtg gcg ggg gac agg ggg ttg gcc ggc tgc ggg cac ctc	48
Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu	
1 5 10 15	
ctg gtc tcg ctg ctg ggg ctg ctg ctg ctg ctg gcg cgc tcc ggc acc	96
Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr	
20 25 30	
cgg gcg ctg gtc tgc ctg ccc tgt gac gag tcc aag tgc gag gag ccc	144
Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro	
35 40 45	
agg aac tgc ccg ggg agc atc gtg cag ggc gtc tgc ggc tgc tgc tac	192
Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr	
50 55 60	
acg tgc gcc agc cag agg aac gag agc tgc ggc ggc acc ttc ggg att	240
Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile	
65 70 75 80	

tac gga acc tgc gac cgg ggg ctg cgt tgt gtc atc cgc ccc ccg ctc	288
Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu	
85 90 95	
aat ggc gac tcc ctc acc gag tac gaa gcg ggc gtt tgc gaa ggt acg	336
Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Gly Thr	
100 105 110	
gcc gcc cgc tgc ggg ccc cct ccc acc tgg cct gcg ccg ccc cct cgg	384
Ala Ala Arg Cys Gly Pro Pro Pro Thr Trp Pro Ala Pro Pro Pro Arg	
115 120 125	
cgc tgg ttg tgc cga aca aag ttt ggg cga gac ttt ctg gag gaa aga	432
Arg Trp Leu Cys Arg Thr Lys Phe Gly Arg Asp Phe Leu Glu Glu Arg	
130 135 140	
ggg ctc tgc ggg aag agg ggc ggc cgc cgc ccc cag gag agt gcc ccc	480
Gly Leu Cys Gly Lys Arg Gly Gly Arg Arg Pro Gln Glu Ser Ala Pro	
145 150 155 160	
gcg gcc ctg cgt tcc ctc tcc ttg ttc ccc ccg acg ctt agg cag tcg	528
Ala Ala Leu Arg Ser Leu Ser Leu Phe Pro Pro Thr Leu Arg Gln Ser	
165 170 175	
cgg gcg agg ttg ggt atg gct gcc tgc ctc cag gaa aat cac cta gaa	576
Arg Ala Arg Leu Gly Met Ala Ala Cys Leu Gln Glu Asn His Leu Glu	
180 185 190	
gcc aga gaa aca agt gtg gat cct gaa ccc ctg aga aag aaa tct gga	624
Ala Arg Glu Thr Ser Val Asp Pro Glu Pro Leu Arg Lys Lys Ser Gly	
195 200 205	
tgg aag aca tct ttg gag gat cga agg cag agt tta gaa aaa tta atg	672
Trp Lys Thr Ser Leu Glu Asp Arg Arg Gln Ser Leu Glu Lys Leu Met	
210 215 220	
aag tga	678
Lys *	
225	

<210> 76

<211> 225

<213> Homo sapiens

[illegible]

<211> 558

<213> Homo sapiens

<221> CDS

<222> (1)...(558)

<400> 77																
atg gcc cgg gcc agg gcc ggg gcg ctg ctg gcg ctt tgg gtg ctc ggg	48															
Met Ala Arg Ala Arg Ala Gly Ala Leu Leu Ala Leu Trp Val Leu Gly																
1 5 10 15																
gcc gcc gcg cat ccg cag tgc ctg gac ttc agg ccg ccc ttc cgg ccg	96															
Ala Ala Ala His Pro Gln Cys Leu Asp Phe Arg Pro Pro Phe Arg Pro																
20 25 30																
acg cag ccg ctg cgc ctc tgc gcg cag tac tcg gac ttc ggc tgc tgc	144															
Thr Gln Pro Leu Arg Leu Cys Ala Gln Tyr Ser Asp Phe Gly Cys Cys																
35 40 45																
gat gag ggg cgc gac gcc gag ctg acc cgc cgc ttc tgg gcc ctg gcg	192															
Asp Glu Gly Arg Asp Ala Glu Leu Thr Arg Arg Phe Trp Ala Leu Ala																
50 55 60																
agc cgc gtg gac gcc gcc gag tgg gcc gcg tgc gcc ggc tac gcg agg	240															
Ser Arg Val Asp Ala Ala Glu Trp Ala Ala Cys Ala Gly Tyr Ala Arg																
65 70 75 80																
gac ctg ctg tgc cag tcc gtg gag tgg aca gac atg caa aga gat aat	288															
Asp Leu Leu Cys Gln Ser Val Glu Trp Thr Asp Met Gln Arg Asp Asn																
85 90 95																
gaa gtc cta gcc aag ctg act ggc tgg agc gcc cct ggc gac gga gca	336															
Glu Val Leu Ala Lys Leu Thr Gly Trp Ser Ala Pro Gly Asp Gly Ala																
100 105 110																
gtg act gct gta gag aac tca ccc tgt aag cta caa gat tca atg gat	384															
Val Thr Ala Val Glu Asn Ser Pro Cys Lys Leu Gln Asp Ser Met Asp																
115 120 125																
tct gga ttg ggc ttt ggt gaa cgg agg gct ctc gtt gcc ttc cag atg	432															
Ser Gly Leu Gly Phe Gly Glu Arg Arg Ala Leu Val Ala Phe Gln Met																
130 135 140																
tct gtt ctg ccc ctc act gcg tct ctg gaa cca aga tgg tgc ctg gta	480															
Ser Val Leu Pro Leu Thr Ala Ser Leu Glu Pro Arg Trp Cys Leu Val																
145 150 155 160																
caa tct ctg ctc agt aaa ttc ttg gtg aat gaa atg ttg ctg act aat	528															

ctg gaa aga aca cca gtc cag gca tca tga
Leu Glu Arg Thr Pro Val Gln Ala Ser *

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<210> 78
<211> 185
<212> PRT
<213> Homo sapiens
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<400> 78															
Met	Ala	Arg	Ala	Arg	Ala	Gly	Ala	Leu	Leu	Ala	Leu	Trp	Val	Leu	Gly
1				5					10					15	
Ala	Ala	Ala	His	Pro	Gln	Cys	Leu	Asp	Phe	Arg	Pro	Pro	Phe	Arg	Pro
			20					25					30		
Thr	Gln	Pro	Leu	Arg	Leu	Cys	Ala	Gln	Tyr	Ser	Asp	Phe	Gly	Cys	Cys
		35					40					45			
Asp	Glu	Gly	Arg	Asp	Ala	Glu	Leu	Thr	Arg	Arg	Phe	Trp	Ala	Leu	Ala
	50					55					60				
Ser	Arg	Val	Asp	Ala	Ala	Glu	Trp	Ala	Ala	Cys	Ala	Gly	Tyr	Ala	Arg
65					70					75					80
Asp	Leu	Leu	Cys	Gln	Ser	Val	Glu	Trp	Thr	Asp	Met	Gln	Arg	Asp	Asn
				85					90					95	
Glu	Val	Leu	Ala	Lys	Leu	Thr	Gly	Trp	Ser	Ala	Pro	Gly	Asp	Gly	Ala
			100					105					110		
Val	Thr	Ala	Val	Glu	Asn	Ser	Pro	Cys	Lys	Leu	Gln	Asp	Ser	Met	Asp
		115					120					125			
Ser	Gly	Leu	Gly	Phe	Gly	Glu	Arg	Arg	Ala	Leu	Val	Ala	Phe	Gln	Met
	130					135					140				
Ser	Val	Leu	Pro	Leu	Thr	Ala	Ser	Leu	Glu	Pro	Arg	Trp	Cys	Leu	Val
145					150					155					160
Gln	Ser	Leu	Leu	Ser	Lys	Phe	Leu	Val	Asn	Glu	Met	Leu	Leu	Thr	Asn
				165					170					175	
Leu	Glu	Arg	Thr	Pro	Val	Gln	Ala	Ser							
			180					185							

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<210> 79
<211> 645
<212> DNA
<213> Homo sapiens
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<220>

<221> CDS

<222> (1)...(645)

<400> 79

atg	ccc	gcg	gcc	cgg	ccg	ccc	gcc	gcg	gga	ctc	cgc	ggg	atc	tcg	ctg	48
Met	Pro	Ala	Ala	Arg	Pro	Pro	Ala	Ala	Gly	Leu	Arg	Gly	Ile	Ser	Leu	
1				5					10					15		

ttc	ctc	gct	ctg	ctc	ctg	ggg	agc	ccg	gcg	gca	gcg	ctg	gag	cga	ggg	96
Phe	Leu	Ala	Leu	Leu	Leu	Gly	Ser	Pro	Ala	Ala	Ala	Leu	Glu	Arg	Gly	
			20					25					30			

gtg	gtc	agt	gaa	ggc	ttc	ctg	gag	cac	gta	gca	ttt	gaa	ctg	gcc	ctg	144
Val	Val	Ser	Glu	Gly	Phe	Leu	Glu	His	Val	Ala	Phe	Glu	Leu	Ala	Leu	
		35					40					45				

aag	ggg	ata	gga	cag	aca	cag	acc	ctg	gag	tcc	aag	aga	tat	ggg	ttc	192
Lys	Gly	Ile	Gly	Gln	Thr	Gln	Thr	Leu	Glu	Ser	Lys	Arg	Tyr	Gly	Phe	
	50					55					60					

aaa	cct	aat	gct	gtg	atc	ttg	aac	aag	tca	ctt	aac	tct	gag	atg	atg	240
Lys	Pro	Asn	Ala	Val	Ile	Leu	Asn	Lys	Ser	Leu	Asn	Ser	Glu	Met	Met	
	65					70				75					80	

gga	gtg	ggt	ggt	agt	gat	gag	gat	gaa	gag	ggg	aat	tat	gag	ttg	ctg	288
Gly	Val	Gly	Gly	Ser	Asp	Glu	Asp	Glu	Glu	Gly	Asn	Tyr	Glu	Leu	Leu	
				85					90					95		

ttg	tta	ctg	atg	gac	cga	gct	gat	tct	cag	aca	ttt	aaa	agt	gat	cca	336
Leu	Leu	Leu	Met	Asp	Arg	Ala	Asp	Ser	Gln	Thr	Phe	Lys	Ser	Asp	Pro	
			100					105					110			

ggc	att	gaa	aat	cag	gtt	gga	gtg	gaa	aat	gaa	gag	aag	cct	caa	ggt	384
Gly	Ile	Glu	Asn	Gln	Val	Gly	Val	Glu	Asn	Glu	Glu	Lys	Pro	Gln	Gly	
		115					120					125				

ggg	gtc	cca	gga	gct	ctc	ccc	ttt	tcc	cat	gag	aga	ttc	atc	tgg	aat	432
Gly	Val	Pro	Gly	Ala	Leu	Pro	Phe	Ser	His	Glu	Arg	Phe	Ile	Trp	Asn	
	130					135					140					

gat	gac	agt	gga	ttt	aag	agc	aat	aag	gga	ggg	gaa	cgg	ctg	agc	cag	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asp Asp Ser Gly Phe Lys Ser Asn Lys Gly Gly Glu Arg Leu Ser Gln
 145 150 155 160

 gga cct gtg gac act cag gat tca act ctg ggc ttg gcc aga gat aag 528
 Gly Pro Val Asp Thr Gln Asp Ser Thr Leu Gly Leu Ala Arg Asp Lys
 165 170 175

 tcc tta gag ttt ggg gca ttt gaa caa ctg aca aga agc cag cat ggc 576
 Ser Leu Glu Phe Gly Ala Phe Glu Gln Leu Thr Arg Ser Gln His Gly
 180 185 190

 cag aat atc ctg aac aga gaa gga agt ggg caa atg aag tta aga gaa 624
 Gln Asn Ile Leu Asn Arg Glu Gly Ser Gly Gln Met Lys Leu Arg Glu
 195 200 205

 agt att aaa gaa aag caa tga 645
 Ser Ile Lys Glu Lys Gln *
 210

<210> 80
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 80
 Met Pro Ala Ala Arg Pro Pro Ala Ala Gly Leu Arg Gly Ile Ser Leu
 1 5 10 15
 Phe Leu Ala Leu Leu Leu Gly Ser Pro Ala Ala Ala Leu Glu Arg Gly
 20 25 30
 Val Val Ser Glu Gly Phe Leu Glu His Val Ala Phe Glu Leu Ala Leu
 35 40 45
 Lys Gly Ile Gly Gln Thr Gln Thr Leu Glu Ser Lys Arg Tyr Gly Phe
 50 55 60
 Lys Pro Asn Ala Val Ile Leu Asn Lys Ser Leu Asn Ser Glu Met Met
 65 70 75 80
 Gly Val Gly Gly Ser Asp Glu Asp Glu Glu Gly Asn Tyr Glu Leu Leu
 85 90 95
 Leu Leu Leu Met Asp Arg Ala Asp Ser Gln Thr Phe Lys Ser Asp Pro
 100 105 110
 Gly Ile Glu Asn Gln Val Gly Val Glu Asn Glu Glu Lys Pro Gln Gly
 115 120 125
 Gly Val Pro Gly Ala Leu Pro Phe Ser His Glu Arg Phe Ile Trp Asn

130 135 140
 Asp Asp Ser Gly Phe Lys Ser Asn Lys Gly Gly Glu Arg Leu Ser Gln
 145 150 155 160
 Gly Pro Val Asp Thr Gln Asp Ser Thr Leu Gly Leu Ala Arg Asp Lys
 165 170 175
 Ser Leu Glu Phe Gly Ala Phe Glu Gln Leu Thr Arg Ser Gln His Gly
 180 185 190
 Gln Asn Ile Leu Asn Arg Glu Gly Ser Gly Gln Met Lys Leu Arg Glu
 195 200 205
 Ser Ile Lys Glu Lys Gln
 210

<210> 81
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(303)

<400> 81
 atg gca gcc ttg ctg ctc ttg acc ctc agc ctg att cag gtc tca ggg 48
 Met Ala Ala Leu Leu Leu Leu Thr Leu Ser Leu Ile Gln Val Ser Gly
 1 5 10 15

 gtg ctg ctg acc tcc agt gtg gac agt ccc tct acc ctg ccg ctg tct 96
 Val Leu Leu Thr Ser Ser Val Asp Ser Pro Ser Thr Leu Pro Leu Ser
 20 25 30

 gca cag aga acc gtc cac cgt ggc ctc ttt aca ttc caa gct gga ttt 144
 Ala Gln Arg Thr Val His Arg Gly Leu Phe Thr Phe Gln Ala Gly Phe
 35 40 45

 tct cct gat cgc tcc agt tct cga ggc aaa aag caa aga gtc tcg ggc 192
 Ser Pro Asp Arg Ser Ser Ser Arg Gly Lys Lys Gln Arg Val Ser Gly
 50 55 60

 tgc aat gac atg gtt tgc ttc ggg ttc tcc ggc gcc gcc tgc ctc ctc 240
 Cys Asn Asp Met Val Cys Phe Gly Phe Ser Gly Ala Ala Cys Leu Leu
 65 70 75 80

 tgt cag atg ccg gtg ttc ggg ggc ggc ttc gtt ggc ttc ctt cct tct 288

Cys Gln Met Pro Val Phe Gly Gly Gly Phe Val Gly Phe Leu Pro Ser
 85 90 95

ctg ttc cag acc taa
 Leu Phe Gln Thr *
 100

303

<210> 82
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 82
 Met Ala Ala Leu Leu Leu Thr Leu Ser Leu Ile Gln Val Ser Gly
 1 5 10 15
 Val Leu Leu Thr Ser Ser Val Asp Ser Pro Ser Thr Leu Pro Leu Ser
 20 25 30
 Ala Gln Arg Thr Val His Arg Gly Leu Phe Thr Phe Gln Ala Gly Phe
 35 40 45
 Ser Pro Asp Arg Ser Ser Ser Arg Gly Lys Lys Gln Arg Val Ser Gly
 50 55 60
 Cys Asn Asp Met Val Cys Phe Gly Phe Ser Gly Ala Ala Cys Leu Leu
 65 70 75 80
 Cys Gln Met Pro Val Phe Gly Gly Gly Phe Val Gly Phe Leu Pro Ser
 85 90 95
 Leu Phe Gln Thr
 100

<210> 83
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1533)

<400> 83
 atg gct tgg gca agt agg ctg ggc ctg ctg ctg gca ctg ctg ctg ccc
 Met Ala Trp Ala Ser Arg Leu Gly Leu Leu Leu Ala Leu Leu Leu Pro
 1 5 10 15

48

gtg gtc ggt gcc tcc acg cca ggc acc gtg gtc cga ctc aac aag gca	96
Val Val Gly Ala Ser Thr Pro Gly Thr Val Val Arg Leu Asn Lys Ala	
20 25 30	
gca ttg agc tac gtg tct gaa att ggg aaa gcc cct ctc cag cgg gcc	144
Ala Leu Ser Tyr Val Ser Glu Ile Gly Lys Ala Pro Leu Gln Arg Ala	
35 40 45	
ctg cag gtc act gtc cct cat ttc ctg gac tgg agt gga gag gcg ctt	192
Leu Gln Val Thr Val Pro His Phe Leu Asp Trp Ser Gly Glu Ala Leu	
50 55 60	
cag ccc acc agg atc cgg att ctg aat gtc cat gtg ccc cgc ctc cac	240
Gln Pro Thr Arg Ile Arg Ile Leu Asn Val His Val Pro Arg Leu His	
65 70 75 80	
ctg aaa ttc att gct ggt ttc gga gtg cgc ctg ctg gca gca gct aat	288
Leu Lys Phe Ile Ala Gly Phe Gly Val Arg Leu Leu Ala Ala Ala Asn	
85 90 95	
ttt act ttc aag gtc ttt cgc gcc cca gag ccc ctg gag ctg acg ctg	336
Phe Thr Phe Lys Val Phe Arg Ala Pro Glu Pro Leu Glu Leu Thr Leu	
100 105 110	
cct gtg gaa ctg ctg gct gac acc cgc gtg acc cag agc tcc atc agg	384
Pro Val Glu Leu Leu Ala Asp Thr Arg Val Thr Gln Ser Ser Ile Arg	
115 120 125	
acc cct gtg gtc agc atc tct gcc tgc tct tta ttc tcg ggc cac gcc	432
Thr Pro Val Val Ser Ile Ser Ala Cys Ser Leu Phe Ser Gly His Ala	
130 135 140	
aac gag ttt gat ggc agt aac agc acc tcc cac gcg ctg ctg gtc ctg	480
Asn Glu Phe Asp Gly Ser Asn Ser Thr Ser His Ala Leu Leu Val Leu	
145 150 155 160	
gtg cag aag cac att aaa gct gtc ttg agt aac aag ctg tgc ctg agc	528
Val Gln Lys His Ile Lys Ala Val Leu Ser Asn Lys Leu Cys Leu Ser	
165 170 175	
atc tcc aac ctg gtg cag ggt gtc aat gtc cac ctg ggc acc tta att	576
Ile Ser Asn Leu Val Gln Gly Val Asn Val His Leu Gly Thr Leu Ile	
180 185 190	

ggc	ctc	aac	ccc	gtg	ggt	cct	gag	tcc	cag	atc	cgc	tat	tcc	atg	gtc	624
Gly	Leu	Asn	Pro	Val	Gly	Pro	Glu	Ser	Gln	Ile	Arg	Tyr	Ser	Met	Val	
		195				200						205				
agt	gtg	ccc	act	gtc	acc	agt	gac	tac	att	tcc	ctg	gaa	gtc	aat	gct	672
Ser	Val	Pro	Thr	Val	Thr	Ser	Asp	Tyr	Ile	Ser	Leu	Glu	Val	Asn	Ala	
		210				215						220				
gtt	ctc	ttc	ctg	ctg	ggc	aag	ccc	atc	atc	ctg	ccc	acg	gat	gcc	acc	720
Val	Leu	Phe	Leu	Leu	Gly	Lys	Pro	Ile	Ile	Leu	Pro	Thr	Asp	Ala	Thr	
225				230						235				240		
cct	ttt	gtg	ttg	cca	agg	cat	gtg	ggt	acc	gag	ggc	tcc	atg	gcc	acc	768
Pro	Phe	Val	Leu	Pro	Arg	His	Val	Gly	Thr	Glu	Gly	Ser	Met	Ala	Thr	
				245				250						255		
gtg	ggc	ctc	tcc	cag	cag	ctg	ttt	gac	tct	gcg	ctc	ctg	ctg	ctg	cag	816
Val	Gly	Leu	Ser	Gln	Gln	Leu	Phe	Asp	Ser	Ala	Leu	Leu	Leu	Leu	Gln	
		260						265				270				
aag	gcc	ggt	gcc	ctc	aac	ctg	gac	atc	aca	ggg	cag	ctg	gtg	gcc	cgc	864
Lys	Ala	Gly	Ala	Leu	Asn	Leu	Asp	Ile	Thr	Gly	Gln	Leu	Val	Ala	Arg	
		275				280						285				
cag	ttt	ccc	gag	ccc	atg	cct	gtg	gtg	ctc	aag	gtg	cgg	ctg	ggt	gcc	912
Gln	Phe	Pro	Glu	Pro	Met	Pro	Val	Val	Leu	Lys	Val	Arg	Leu	Gly	Ala	
290						295				300						
aca	cct	gtg	gcc	atg	ctc	cac	aca	aac	aac	gcc	acc	ctg	cgg	ctg	cag	960
Thr	Pro	Val	Ala	Met	Leu	His	Thr	Asn	Asn	Ala	Thr	Leu	Arg	Leu	Gln	
305				310						315				320		
ccc	ttc	gtg	gag	gtc	ctg	gcc	aca	gcc	tcc	aac	tcg	gct	ttc	cag	tcc	1008
Pro	Phe	Val	Glu	Val	Leu	Ala	Thr	Ala	Ser	Asn	Ser	Ala	Phe	Gln	Ser	
				325				330						335		
ctc	ttc	tcc	ctg	gat	gtg	gta	gtg	aac	ttg	aga	ctc	cag	ctc	tct	gtg	1056
Leu	Phe	Ser	Leu	Asp	Val	Val	Val	Asn	Leu	Arg	Leu	Gln	Leu	Ser	Val	
		340				345						350				
tcc	aag	gtg	aag	ctt	cag	ggg	acc	acg	tct	gtg	ctg	ggg	gat	gtc	cag	1104
Ser	Lys	Val	Lys	Leu	Gln	Gly	Thr	Thr	Ser	Val	Leu	Gly	Asp	Val	Gln	

<210> 84
<211> 510
<212> PRT
<213> Homo sapiens

Met 1	Ala	Trp	Ala	Ser 5	Arg	Leu	Gly	Leu	Leu 10	Leu	Ala	Leu	Leu	Leu 15	Pro
Val	Val	Gly	Ala 20	Ser	Thr	Pro	Gly	Thr	Val	Val	Arg	Leu	Asn 30	Lys	Ala
Ala	Leu	Ser	Tyr	Val	Ser	Glu	Ile 40	Gly	Lys	Ala	Pro	Leu	Gln	Arg	Ala
Leu	Gln 50	Val	Thr	Val	Pro	His 55	Phe	Leu	Asp	Trp	Ser 60	Gly	Glu	Ala	Leu
Gln 65	Pro	Thr	Arg	Ile	Arg	Ile 70	Leu	Asn	Val	His 75	Val	Pro	Arg	Leu	His
Leu	Lys	Phe	Ile	Ala 85	Gly	Phe	Gly	Val	Arg 90	Leu	Leu	Ala	Ala	Ala 95	Asn
Phe	Thr	Phe	Lys 100	Val	Phe	Arg	Ala	Pro 105	Glu	Pro	Leu	Glu	Leu	Thr	Leu
Pro	Val	Glu	Leu 115	Leu	Ala	Asp	Thr	Arg 120	Val	Thr	Gln	Ser	Ser	Ile	Arg
Thr	Pro 130	Val	Val	Ser	Ile	Ser 135	Ala	Cys	Ser	Leu	Phe 140	Ser	Gly	His	Ala
Asn 145	Glu	Phe	Asp	Gly	Ser 150	Asn	Ser	Thr	Ser	His 155	Ala	Leu	Leu	Val	Leu
Val	Gln	Lys	His 165	Ile	Lys	Ala	Val	Leu	Ser 170	Asn	Lys	Leu	Cys	Leu	Ser
Ile	Ser	Asn 180	Leu	Val	Gln	Gly	Val	Asn 185	Val	His	Leu	Gly	Thr	Leu	Ile
Gly	Leu 195	Asn	Pro	Val	Gly	Pro	Glu	Ser 200	Gln	Ile	Arg	Tyr	Ser	Met	Val
Ser	Val 210	Pro	Thr	Val	Thr	Ser	Asp	Tyr 215	Ile	Ser	Leu	Glu	Val	Asn	Ala
Val 225	Leu	Phe	Leu	Leu	Gly	Lys 230	Pro	Ile	Ile	Leu	Pro	Thr	Asp	Ala	Thr
Pro	Phe	Val	Leu 245	Pro	Arg	His	Val	Gly	Thr 250	Glu	Gly	Ser	Met	Ala	Thr
Val	Gly	Leu	Ser 260	Gln	Gln	Leu	Phe	Asp 265	Ser	Ala	Leu	Leu	Leu	Leu	Gln
Lys	Ala 275	Gly	Ala	Leu	Asn	Leu	Asp	Ile 280	Thr	Gly	Gln	Leu	Val	Ala	Arg
Gln	Phe 290	Pro	Glu	Pro	Met	Pro 295	Val	Val	Leu	Lys	Val 300	Arg	Leu	Gly	Ala
Thr 305	Pro	Val	Ala	Met	Leu	His 310	Thr	Asn	Asn	Ala 315	Thr	Leu	Arg	Leu	Gln
Pro	Phe	Val	Glu	Val	Leu	Ala	Thr	Ala	Ser	Asn	Ser	Ala	Phe	Gln	Ser

325 330 335
 Leu Phe Ser Leu Asp Val Val Val Asn Leu Arg Leu Gln Leu Ser Val
 340 345 350
 Ser Lys Val Lys Leu Gln Gly Thr Thr Ser Val Leu Gly Asp Val Gln
 355 360 365
 Leu Thr Val Ala Ser Ser Asn Val Gly Phe Ile Asp Pro Ser Pro Gln
 370 375 380
 Lys Ser Ile Gly Gln Leu Asp Lys Glu Cys Gln Leu Ser Leu Gln Pro
 385 390 395 400
 Gly Asp Val Ile Gly Ser Ser Ala Thr Ile His Pro Leu Val Ser Arg
 405 410 415
 His Ala Ile Asn Met Pro Pro Phe Tyr Pro Ala Val Ser Leu Ser Val
 420 425 430
 Cys Arg Ser Ser Ala Ser Gly Ser Leu Leu Ala Ser Pro Pro Val Gly
 435 440 445
 His Thr Thr Asp Gln Val Arg Thr Leu Met Gly Thr Val Phe Glu Lys
 450 455 460
 Pro Leu Leu Asp His Leu Asn Ala Leu Leu Ala Met Gly Ile Ala Leu
 465 470 475 480
 Pro Gly Val Val Asn Leu His Tyr Val Ala Pro Glu Ile Phe Val Tyr
 485 490 495
 Glu Gly Tyr Val Val Ile Ser Ser Gly Leu Phe Tyr Gln Ser
 500 505 510

<210> 85
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(453)

<400> 85

atg gct gtc ctg gtg gtc tct ctt ggg tcc ctc gct cta ggg gaa gaa 48
 Met Ala Val Leu Val Val Ser Leu Gly Ser Leu Ala Leu Gly Glu Glu
 1 5 10 15

gtc ctg tta gtg gcc cca tgg aga ggc cca cac agc aag gaa ctg aag 96
 Val Leu Leu Val Ala Pro Trp Arg Gly Pro His Ser Lys Glu Leu Lys
 20 25 30

ctt cct gcc cac agc aac gag aga aag ctt aga ggt agc cct cag gtc 144

Leu Pro Ala His Ser Asn Glu Arg Lys Leu Arg Gly Ser Pro Gln Val
 35 40 45
 cca gcc aag tct tca gag ccg gcc act ctg gcc aac agc ttg agt aca 192
 Pro Ala Lys Ser Ser Glu Pro Ala Thr Leu Ala Asn Ser Leu Ser Thr
 50 55 60
 act gca cgc aag ccg caa gcc gga acc act ggg cta gga tgc tcc cag 240
 Thr Ala Arg Lys Pro Gln Ala Gly Thr Thr Gly Leu Gly Cys Ser Gln
 65 70 75 80
 att ctg agc tct gag gat ttg act cag gca aag att att gct gct ggc 288
 Ile Leu Ser Ser Glu Asp Leu Thr Gln Ala Lys Ile Ile Ala Ala Gly
 85 90 95
 aga agg tcg agg caa aaa ttc tct acc ttg gag gga agg gtg gat aca 336
 Arg Arg Ser Arg Gln Lys Phe Ser Thr Leu Glu Gly Arg Val Asp Thr
 100 105 110
 gat atc aaa cag atg tct agt ctt gct agg aat ggg gcc gaa aac tcc 384
 Asp Ile Lys Gln Met Ser Ser Leu Ala Arg Asn Gly Ala Glu Asn Ser
 115 120 125
 cac cct acg cca acc atg gac aca agg aga agt ttg gca gcc aca ggt 432
 His Pro Thr Pro Thr Met Asp Thr Arg Arg Ser Leu Ala Ala Thr Gly
 130 135 140
 aga agg agc aag aat gct tag 453
 Arg Arg Ser Lys Asn Ala *
 145 150

<210> 86

<211> 150

<212> PRT

<213> Homo sapiens

<400> 86

Met Ala Val Leu Val Val Ser Leu Gly Ser Leu Ala Leu Gly Glu Glu
 1 5 10 15
 Val Leu Leu Val Ala Pro Trp Arg Gly Pro His Ser Lys Glu Leu Lys
 20 25 30
 Leu Pro Ala His Ser Asn Glu Arg Lys Leu Arg Gly Ser Pro Gln Val

35 40 45
 Pro Ala Lys Ser Ser Glu Pro Ala Thr Leu Ala Asn Ser Leu Ser Thr
 50 55 60
 Thr Ala Arg Lys Pro Gln Ala Gly Thr Thr Gly Leu Gly Cys Ser Gln
 65 70 75 80
 Ile Leu Ser Ser Glu Asp Leu Thr Gln Ala Lys Ile Ile Ala Ala Gly
 85 90 95
 Arg Arg Ser Arg Gln Lys Phe Ser Thr Leu Glu Gly Arg Val Asp Thr
 100 105 110
 Asp Ile Lys Gln Met Ser Ser Leu Ala Arg Asn Gly Ala Glu Asn Ser
 115 120 125
 His Pro Thr Pro Thr Met Asp Thr Arg Arg Ser Leu Ala Ala Thr Gly
 130 135 140
 Arg Arg Ser Lys Asn Ala
 145 150

<210> 87

<211> 438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(438)

<400> 87

atg ggc cgc cgc cgc ctg ctc gtc tgg ctg tgc gcc gtc gcg gcg ctg 48
 Met Gly Arg Arg Arg Leu Leu Val Trp Leu Cys Ala Val Ala Ala Leu
 1 5 10 15

ctc tcg ggg gcg cag gcc agg ggc acc ccg ctc ctg gcg cgg cct gcg 96
 Leu Ser Gly Ala Gln Ala Arg Gly Thr Pro Leu Leu Ala Arg Pro Ala
 20 25 30

ccg ccc ggt gcc tcc cgc tac agt ctc tac acg acg gga tgg cgc ccg 144
 Pro Pro Gly Ala Ser Arg Tyr Ser Leu Tyr Thr Thr Gly Trp Arg Pro
 35 40 45

cgg ctg cgc ccg ggg ccg cac aag gcc ctc tgt gcc tat gtg gtg cac 192
 Arg Leu Arg Pro Gly Pro His Lys Ala Leu Cys Ala Tyr Val Val His
 50 55 60

agg aat gtg acc tgc atc cta cag gag gga gcg gag agc tac gta aag 240

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<210> 88
<211> 145
<212> PRT
<213> Homo sapiens

<400> 88
Met Gly Arg Arg Arg Leu Leu Val Trp Leu Cys Ala Val Ala Ala Leu
 1          5          10          15
Leu Ser Gly Ala Gln Ala Arg Gly Thr Pro Leu Leu Ala Arg Pro Ala
          20          25          30
Pro Pro Gly Ala Ser Arg Tyr Ser Leu Tyr Thr Thr Gly Trp Arg Pro
          35          40          45
Arg Leu Arg Pro Gly Pro His Lys Ala Leu Cys Ala Tyr Val Val His
          50          55          60
Arg Asn Val Thr Cys Ile Leu Gln Glu Gly Ala Glu Ser Tyr Val Lys
65          70          75          80
Ala Glu Tyr Arg Gln Cys Arg Trp Gly Pro Lys Cys Pro Gly Thr Val
          85          90          95
Thr Pro Gln Thr Ala Tyr Ala Phe Arg Leu Gln Glu Arg Leu Ser Ser

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100 105 110
 Gly Ser Ala Ser His Ala Glu Tyr Arg Gly Ser His Asp Ser Ile Asn
 115 120 125
 Arg Gly Leu Gly Ser Leu Arg Cys Ala Arg Met Tyr Ala Gln Leu Val
 130 135 140
 Ile
 145

<210> 89
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(372)

<400> 89

atg ctg ctg ctg ctc ctg ttg ctg ctg ctg cta cag ctc cag gcc ctt 48
 Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Gln Leu Gln Ala Leu
 1 5 10 15

gct ctg gtg cca ctg gag caa aat ctc tcc cca aga ccc cgg gtg aag 96
 Ala Leu Val Pro Leu Glu Gln Asn Leu Ser Pro Arg Pro Arg Val Lys
 20 25 30

agt gct gct cca aca caa caa cca gtc acc tgc ttg ctg agg att ggt 144
 Ser Ala Ala Pro Thr Gln Gln Pro Val Thr Cys Leu Leu Arg Ile Gly
 35 40 45

tgt cat gct cct gct tgg ccc aca agc atc tcc cac aag aaa ttc tgc 192
 Cys His Ala Pro Ala Trp Pro Thr Ser Ile Ser His Lys Lys Phe Cys
 50 55 60

agg aaa tcc agg gtc ctg tct gaa ccc aaa gat gtt tct atc tat cga 240
 Arg Lys Ser Arg Val Leu Ser Glu Pro Lys Asp Val Ser Ile Tyr Arg
 65 70 75 80

atg ttc cct ggt cat tgg ttg aag gcc atc aag tcg gcg gtg aaa gtc 288
 Met Phe Pro Gly His Trp Leu Lys Ala Ile Lys Ser Ala Val Lys Val
 85 90 95

tta ccc agt act tac aca gta ctt cag ctt agc tgc gaa aat atc aat 336

Leu Pro Ser Thr Tyr Thr Val Leu Gln Leu Ser Cys Glu Asn Ile Asn
 100 105 110

gag ctg ccg aac tgt gtg gac ccc aag cca ggc tga 372
 Glu Leu Pro Asn Cys Val Asp Pro Lys Pro Gly *
 115 120

<210> 90
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 90
 Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Gln Leu Gln Ala Leu
 1 5 10 15
 Ala Leu Val Pro Leu Glu Gln Asn Leu Ser Pro Arg Pro Arg Val Lys
 20 25 30
 Ser Ala Ala Pro Thr Gln Gln Pro Val Thr Cys Leu Leu Arg Ile Gly
 35 40 45
 Cys His Ala Pro Ala Trp Pro Thr Ser Ile Ser His Lys Lys Phe Cys
 50 55 60
 Arg Lys Ser Arg Val Leu Ser Glu Pro Lys Asp Val Ser Ile Tyr Arg
 65 70 75 80
 Met Phe Pro Gly His Trp Leu Lys Ala Ile Lys Ser Ala Val Lys Val
 85 90 95
 Leu Pro Ser Thr Tyr Thr Val Leu Gln Leu Ser Cys Glu Asn Ile Asn
 100 105 110
 Glu Leu Pro Asn Cys Val Asp Pro Lys Pro Gly
 115 120

<210> 91
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(618)

<400> 91
 atg gag ttg ctg tta ctg gcg gtg ttg agt cgg ggg act ggg gca gtt 48
 Met Glu Leu Leu Leu Leu Ala Val Leu Ser Arg Gly Thr Gly Ala Val

1					5					10					15					
gca	ctg	ctg	tct	gac	tgc	att	ttc	aaa	ggg	cag	cag	tgc	tgt	gct	ggg		96			
Ala	Leu	Leu	Ser	Asp	Cys	Ile	Phe	Lys	Gly	Gln	Gln	Cys	Cys	Ala	Gly					
			20					25					30							
ggc	ctg	ctc	cag	tcc	cta	gtc	acc	tcg	tac	tcc	cta	aat	gct	gaa	ggc		144			
Gly	Leu	Leu	Gln	Ser	Leu	Val	Thr	Ser	Tyr	Ser	Leu	Asn	Ala	Glu	Gly					
			35					40					45							
aaa	caa	cag	cta	agg	ctg	caa	aac	agc	aaa	gat	gat	gac	ctg	ccc	ctc		192			
Lys	Gln	Gln	Leu	Arg	Leu	Gln	Asn	Ser	Lys	Asp	Asp	Asp	Leu	Pro	Leu					
			50					55					60							
cct	ctg	gga	gct	cca	acc	cac	ggg	ggg	atg	ggg	ctg	ctg	aaa	aca	cca		240			
Pro	Leu	Gly	Ala	Pro	Thr	His	Gly	Gly	Met	Gly	Leu	Leu	Lys	Thr	Pro					
			65					70					75		80					
gca	aag	ggc	gac	tgg	aga	ccc	tgg	tcc	tgc	cca	aat	tcg	gct	gtg	aat		288			
Ala	Lys	Gly	Asp	Trp	Arg	Pro	Trp	Ser	Cys	Pro	Asn	Ser	Ala	Val	Asn					
			85					90					95							
cca	tct	ggc	cct	gga	ctc	ttt	ttg	gtt	ggc	aaa	cta	ttg	att	att	gcc		336			
Pro	Ser	Gly	Pro	Gly	Leu	Phe	Leu	Val	Gly	Lys	Leu	Leu	Ile	Ile	Ala					
			100					105					110							
aca	att	tca	gag	cct	gtt	att	ggc	cta	ttc	aga	gat	tca	act	tct	tcc		384			
Thr	Ile	Ser	Glu	Pro	Val	Ile	Gly	Leu	Phe	Arg	Asp	Ser	Thr	Ser	Ser					
			115					120					125							
tgg	ttt	agt	ctt	ggg	aga	gtg	tat	gtg	tcg	agg	aat	gta	tcc	att	tct		432			
Trp	Phe	Ser	Leu	Gly	Arg	Val	Tyr	Val	Ser	Arg	Asn	Val	Ser	Ile	Ser					
			130					135					140							
tac	aac	gga	tgt	gaa	gga	cct	ctt	caa	gga	gaa	cta	caa	acc	act	gct		480			
Tyr	Asn	Gly	Cys	Glu	Gly	Pro	Leu	Gln	Gly	Glu	Leu	Gln	Thr	Thr	Ala					
			145					150					155		160					
caa	gga	aat	aaa	aga	gga	cac	aaa	caa	atg	gaa	gaa	cat	tcc	atg	ctc		528			
Gln	Gly	Asn	Lys	Arg	Gly	His	Lys	Gln	Met	Glu	Glu	His	Ser	Met	Leu					
			165					170					175							
atg	ggc	agg	aag	aat	caa	tat	cgt	gaa	aat	ggc	cat	act	gcc	caa	gac		576			

ctc cag gac tgt gat gag agg ggc tac tgc caa gat ctc tga 618
Leu Gln Asp Cys Asp Glu Arg Gly Tyr Cys Gln Asp Leu *
195 200 205

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<210> 92
<211> 205
<212> PRT
<213> Homo sapiens
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<400> 92															
Met	Glu	Leu	Leu	Leu	Leu	Ala	Val	Leu	Ser	Arg	Gly	Thr	Gly	Ala	Val
1				5					10					15	
Ala	Leu	Leu	Ser	Asp	Cys	Ile	Phe	Lys	Gly	Gln	Gln	Cys	Cys	Ala	Gly
			20					25					30		
Gly	Leu	Leu	Gln	Ser	Leu	Val	Thr	Ser	Tyr	Ser	Leu	Asn	Ala	Glu	Gly
		35					40					45			
Lys	Gln	Gln	Leu	Arg	Leu	Gln	Asn	Ser	Lys	Asp	Asp	Asp	Leu	Pro	Leu
		50				55					60				
Pro	Leu	Gly	Ala	Pro	Thr	His	Gly	Gly	Met	Gly	Leu	Leu	Lys	Thr	Pro
65					70					75					80
Ala	Lys	Gly	Asp	Trp	Arg	Pro	Trp	Ser	Cys	Pro	Asn	Ser	Ala	Val	Asn
				85					90					95	
Pro	Ser	Gly	Pro	Gly	Leu	Phe	Leu	Val	Gly	Lys	Leu	Leu	Ile	Ile	Ala
			100					105					110		
Thr	Ile	Ser	Glu	Pro	Val	Ile	Gly	Leu	Phe	Arg	Asp	Ser	Thr	Ser	Ser
		115					120					125			
Trp	Phe	Ser	Leu	Gly	Arg	Val	Tyr	Val	Ser	Arg	Asn	Val	Ser	Ile	Ser
	130					135					140				
Tyr	Asn	Gly	Cys	Glu	Gly	Pro	Leu	Gln	Gly	Glu	Leu	Gln	Thr	Thr	Ala
145					150					155					160
Gln	Gly	Asn	Lys	Arg	Gly	His	Lys	Gln	Met	Glu	Glu	His	Ser	Met	Leu
				165					170					175	
Met	Gly	Arg	Lys	Asn	Gln	Tyr	Arg	Glu	Asn	Gly	His	Thr	Ala	Gln	Asp
			180					185					190		
Leu	Gln	Asp	Cys	Asp	Glu	Arg	Gly	Tyr	Cys	Gln	Asp	Leu			
		195					200					205			

$\langle 210 \rangle$	93
$\langle 211 \rangle$	342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(342)

<400> 93

atg gcg gcg gcc cca cgc gcg ggc cgg cgg cgc ggg cag ccg ctc ctg	48
Met Ala Ala Ala Pro Arg Ala Gly Arg Arg Arg Gly Gln Pro Leu Leu	
1 5 10 15	

gcg ctg ctg ctt ctg ctg ctg gcg cca ctg ccg ccg ggg gcc ccg ccg	96
Ala Leu Leu Leu Leu Leu Leu Ala Pro Leu Pro Pro Gly Ala Pro Pro	
20 25 30	

ggc gcc gac gcc tac ttc ccc gag gag cgc tgg agc ccg gag tcg ccc	144
Gly Ala Asp Ala Tyr Phe Pro Glu Glu Arg Trp Ser Pro Glu Ser Pro	
35 40 45	

ctg cag gcg ccg cgc gtg ctc atc gcg ctg ttg gcg cga aac gcg gcc	192
Leu Gln Ala Pro Arg Val Leu Ile Ala Leu Leu Ala Arg Asn Ala Ala	
50 55 60	

cac gcg ttg ccc acc acg ctg ggc gca ctc gag cgg ctg cgg cac ccg	240
His Ala Leu Pro Thr Thr Leu Gly Ala Leu Glu Arg Leu Arg His Pro	
65 70 75 80	

cgg gag cgc acg gcg cta tgg acg gag ccc aga gcc ccc act ggg gcg	288
Arg Glu Arg Thr Ala Leu Trp Thr Glu Pro Arg Ala Pro Thr Gly Ala	
85 90 95	

ttg cca gag gcc aca tct aac agc aag cct ttc tgt gcc ggc tgc tgc	336
Leu Pro Glu Ala Thr Ser Asn Ser Lys Pro Phe Cys Ala Gly Cys Cys	
100 105 110	

cct taa	342
Pro *	

<210> 94

<211> 113

<213> Homo sapiens

[illegible]

<211> 343

<213> Homo sapiens

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (343)$

atg	aca	gca	agc	cgc	cag	atg	ttt	aga	ctt	tct	gtt	ctc	ctt	gct	ggc	48
Met	Thr	Ala	Ser	Arg	Gln	Met	Phe	Arg	Leu	Ser	Val	Leu	Leu	Ala	Gly	
1				5					10					15		
.																
tct	gta	ttg	cca	gcc	ctg	gct	act	gct	gtt	aga	aac	ctt	tct	gag	act	96
Ser	Val	Leu	Pro	Ala	Leu	Ala	Thr	Ala	Val	Arg	Asn	Leu	Ser	Glu	Thr	
			20					25					30			
.																
aga	cca	gtt	aaa	ctt	gtg	gtt	ccg	tgg	gtt	gat	atc	cag	aaa	tta	gaa	144
Arg	Pro	Val	Lys	Leu	Val	Val	Pro	Trp	Val	Asp	Ile	Gln	Lys	Leu	Glu	
			35				40					45				

[illegible]

<210> 97
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(420)

<400> 97

atg ctg ctg ctg ctg ctg ttg ttt atg aga cag ggt ctg gct ctg tca	48
Met Leu Leu Leu Leu Leu Leu Phe Met Arg Gln Gly Leu Ala Leu Ser	
1 5 10 15	
ccc agc ctg gag tgc agt gac gtc atc att gcc cac tgc agc ctc agc	96
Pro Ser Leu Glu Cys Ser Asp Val Ile Ile Ala His Cys Ser Leu Ser	
20 25 30	
ctc gtg ggc tcg agt gat cct cct gaa aca aca tat att ggc acc ctc	144
Leu Val Gly Ser Ser Asp Pro Pro Glu Thr Thr Tyr Ile Gly Thr Leu	
35 40 45	
ctt gtg tct gtg aat cca tac cag gag ctc gga atc tac act gtg ctg	192
Leu Val Ser Val Asn Pro Tyr Gln Glu Leu Gly Ile Tyr Thr Val Leu	
50 55 60	
tgc aag tcc aag aac att atc ctg agg gaa tgc ttc ctg ctg gcc gag	240
Cys Lys Ser Lys Asn Ile Ile Leu Arg Glu Cys Phe Leu Leu Ala Glu	
65 70 75 80	
tta gaa aac cgg agg agg ccc cca aca ggc ttg tcc aat aag ggt gtg	288
Leu Glu Asn Arg Arg Arg Pro Pro Thr Gly Leu Ser Asn Lys Gly Val	
85 90 95	
gcc tat ctc cct act gga cct ctt ctg gag gga gcc tca acg ccc aaa	336
Ala Tyr Leu Pro Thr Gly Pro Leu Leu Glu Gly Ala Ser Thr Pro Lys	
100 105 110	
aga cct aat aac aac aat aaa att gtg ggc aca ttg cca atg atg gga	384
Arg Pro Asn Asn Asn Asn Lys Ile Val Gly Thr Leu Pro Met Met Gly	
115 120 125	

420

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<210> 98
<211> 139
<212> PRT
<213> Homo sapiens
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<400> 98															
Met	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Met	Arg	Gln	Gly	Leu	Ala	Leu	Ser
1				5				10						15	
Pro	Ser	Leu	Glu	Cys	Ser	Asp	Val	Ile	Ile	Ala	His	Cys	Ser	Leu	Ser
			20					25					30		
Leu	Val	Gly	Ser	Ser	Asp	Pro	Pro	Glu	Thr	Thr	Tyr	Ile	Gly	Thr	Leu
		35					40					45			
Leu	Val	Ser	Val	Asn	Pro	Tyr	Gln	Glu	Leu	Gly	Ile	Thr	Thr	Val	Leu
	50					55					60				
Cys	Lys	Ser	Lys	Asn	Ile	Ile	Leu	Arg	Glu	Cys	Phe	Leu	Leu	Ala	Glu
65				70						75					80
Leu	Glu	Asn	Arg	Arg	Arg	Pro	Pro	Thr	Gly	Leu	Ser	Asn	Lys	Gly	Val
				85					90					95	
Ala	Tyr	Leu	Pro	Thr	Gly	Pro	Leu	Leu	Glu	Gly	Ala	Ser	Thr	Pro	Lys
			100					105					110		
Arg	Pro	Asn	Asn	Asn	Asn	Lys	Ile	Val	Gly	Thr	Leu	Pro	Met	Met	Gly
		115					120					125			
Gly	Gly	Ser	Pro	Lys	Ala	Gln	Glu	Trp	Ser	Trp					
	130					135									

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<210> 99
<211> 2172
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(2172)

<400> 99
atg gct ctc agc ctc tgg ccc ctg ctg ctg ctg ctg ctg ctg ctg ctg
Met Ala Leu Ser Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

cct tct ctg ctg ctg ttg tta gag ggc aca cgc tgg caa gct ctg gtg 576
Pro Ser Leu Leu Leu Leu Leu Glu Gly Thr Arg Trp Gln Ala Leu Val

180	185	190	
cag gtg cag ccc agt gtg gac ccc acc aat gcc aca ggc ctc gat ggg Gln Val Gln Pro Ser Val Asp Pro Thr Asn Ala Thr Gly Leu Asp Gly 195 200 205			624
agg gag gca gct cct cac ttt ttg cag ggt ctg ttg ggt ttg ctt acc Arg Glu Ala Ala Pro His Phe Leu Gln Gly Leu Leu Gly Leu Leu Thr 210 215 220			672
cca aca ggg gag cta ggc tcc aag gag gct ctt tgg ggc ggt ctg cta Pro Thr Gly Glu Leu Gly Ser Lys Glu Ala Leu Trp Gly Gly Leu Leu 225 230 235 240			720
cgc aca gtg ggg gcc ccc ctc tat gct gcc ttt cag gag ggg ctg ctc Arg Thr Val Gly Ala Pro Leu Tyr Ala Ala Phe Gln Glu Gly Leu Leu 245 250 255			768
cgt gtc act cac tcc ctg cag gat gag gtc ttc tcc att ttg ggg cag Arg Val Thr His Ser Leu Gln Asp Glu Val Phe Ser Ile Leu Gly Gln 260 265 270			816
cca gag cct gat acc aat ggg cag tgc cag gga ggt aac ctt caa cag Pro Glu Pro Asp Thr Asn Gly Gln Cys Gln Gly Gly Asn Leu Gln Gln 275 280 285			864
ctg ctc tta tgg ggc gtc cgg cac aac ctt tcc tgg gat gtc cag gcg Leu Leu Leu Trp Gly Val Arg His Asn Leu Ser Trp Asp Val Gln Ala 290 295 300			912
ctg ggc ttt ctg tct gga tca cca ccc cca ccc cct gcc ctc ctt cac Leu Gly Phe Leu Ser Gly Ser Pro Pro Pro Pro Pro Ala Leu Leu His 305 310 315 320			960
tgc ctg agc acg ggc gtg cct ctg ccc aga gct tct cag ccg tca gcc Cys Leu Ser Thr Gly Val Pro Leu Pro Arg Ala Ser Gln Pro Ser Ala 325 330 335			1008
cac atc agc cca cgc caa cgg cga gcc atc act gtg gag gcc ctc tgt His Ile Ser Pro Arg Gln Arg Arg Ala Ile Thr Val Glu Ala Leu Cys 340 345 350			1056
gag aac cac tta ggc cca gca cca ccc tac agc att tcc aac ttc tcc			1104

Glu	Asn	His	Leu	Gly	Pro	Ala	Pro	Tyr	Ser	Ile	Ser	Asn	Phe	Ser		
		355					360				365					
atc	cac	ttg	ctc	tgc	cag	cac	acc	aag	cct	gcc	act	cca	cag	ccc	cat	1152
Ile	His	Leu	Leu	Cys	Gln	His	Thr	Lys	Pro	Ala	Thr	Pro	Gln	Pro	His	
	370					375					380					
ccc	agc	acc	act	gcc	atc	tgc	cag	aca	gct	gtg	tgg	tat	gca	gtg	tcc	1200
Pro	Ser	Thr	Thr	Ala	Ile	Cys	Gln	Thr	Ala	Val	Trp	Tyr	Ala	Val	Ser	
385					390					395					400	
tgg	gca	cca	ggc	gcc	caa	ggc	tgg	cta	cag	gcc	tgc	cac	gac	cag	ttt	1248
Trp	Ala	Pro	Gly	Ala	Gln	Gly	Trp	Leu	Gln	Ala	Cys	His	Asp	Gln	Phe	
				405					410					415		
cct	gat	gag	ttt	ttg	gat	gcg	atc	tgc	agt	aac	ctc	tcc	ttt	tca	gcc	1296
Pro	Asp	Glu	Phe	Leu	Asp	Ala	Ile	Cys	Ser	Asn	Leu	Ser	Phe	Ser	Ala	
			420					425					430			
ctg	tct	ggc	tcc	aac	cgc	cgc	ctg	gtg	aag	cgg	ctc	tgt	gct	ggc	ctg	1344
Leu	Ser	Gly	Ser	Asn	Arg	Arg	Leu	Val	Lys	Arg	Leu	Cys	Ala	Gly	Leu	
		435					440					445				
ctc	cca	ccc	cct	acc	agc	tgc	cct	gaa	ggc	ctg	ccc	cct	gtt	ccc	ctc	1392
Leu	Pro	Pro	Pro	Thr	Ser	Cys	Pro	Glu	Gly	Leu	Pro	Pro	Val	Pro	Leu	
	450					455					460					
acc	cca	gac	atc	ttt	tgg	ggc	tgc	ttc	ttg	gag	aat	gag	act	ctg	tgg	1440
Thr	Pro	Asp	Ile	Phe	Trp	Gly	Cys	Phe	Leu	Glu	Asn	Glu	Thr	Leu	Trp	
465					470				475					480		
gct	gag	cga	ctg	tgt	ggg	gag	gca	agt	cta	cag	gct	gtg	ccc	ccc	agc	1488
Ala	Glu	Arg	Leu	Cys	Gly	Glu	Ala	Ser	Leu	Gln	Ala	Val	Pro	Pro	Ser	
				485				490						495		
aac	cag	gct	tgg	gtc	cag	cat	gtg	tgc	cag	ggc	ccc	acc	cca	gat	gtc	1536
Asn	Gln	Ala	Trp	Val	Gln	His	Val	Cys	Gln	Gly	Pro	Thr	Pro	Asp	Val	
			500					505					510			
act	gcc	tcc	cca	cca	tgc	cac	att	gga	ccc	tgt	ggg	gaa	cgc	tgc	ccg	1584
Thr	Ala	Ser	Pro	Pro	Cys	His	Ile	Gly	Pro	Cys	Gly	Glu	Arg	Cys	Pro	
		515					520					525				

210	215	220
Pro Thr Gly Glu Leu Gly Ser Lys Glu Ala Leu Trp Gly Gly Leu Leu		
225	230	235
Arg Thr Val Gly Ala Pro Leu Tyr Ala Ala Phe Gln Glu Gly Leu Leu		240
	245	250
Arg Val Thr His Ser Leu Gln Asp Glu Val Phe Ser Ile Leu Gly Gln		255
	260	265
Pro Glu Pro Asp Thr Asn Gly Gln Cys Gln Gly Gly Asn Leu Gln Gln		270
	275	280
Leu Leu Leu Trp Gly Val Arg His Asn Leu Ser Trp Asp Val Gln Ala		285
	290	295
Leu Gly Phe Leu Ser Gly Ser Pro Pro Pro Pro Pro Ala Leu Leu His		300
305	310	315
Cys Leu Ser Thr Gly Val Pro Leu Pro Arg Ala Ser Gln Pro Ser Ala		320
	325	330
His Ile Ser Pro Arg Gln Arg Arg Ala Ile Thr Val Glu Ala Leu Cys		335
	340	345
Glu Asn His Leu Gly Pro Ala Pro Pro Tyr Ser Ile Ser Asn Phe Ser		350
	355	360
Ile His Leu Leu Cys Gln His Thr Lys Pro Ala Thr Pro Gln Pro His		365
	370	375
Pro Ser Thr Thr Ala Ile Cys Gln Thr Ala Val Trp Tyr Ala Val Ser		380
385	390	395
Trp Ala Pro Gly Ala Gln Gly Trp Leu Gln Ala Cys His Asp Gln Phe		400
	405	410
Pro Asp Glu Phe Leu Asp Ala Ile Cys Ser Asn Leu Ser Phe Ser Ala		415
	420	425
Leu Ser Gly Ser Asn Arg Arg Leu Val Lys Arg Leu Cys Ala Gly Leu		430
	435	440
Leu Pro Pro Pro Thr Ser Cys Pro Glu Gly Leu Pro Pro Val Pro Leu		445
	450	455
Thr Pro Asp Ile Phe Trp Gly Cys Phe Leu Glu Asn Glu Thr Leu Trp		460
465	470	475
Ala Glu Arg Leu Cys Gly Glu Ala Ser Leu Gln Ala Val Pro Pro Ser		480
	485	490
Asn Gln Ala Trp Val Gln His Val Cys Gln Gly Pro Thr Pro Asp Val		495
	500	505
Thr Ala Ser Pro Pro Cys His Ile Gly Pro Cys Gly Glu Arg Cys Pro		510
	515	520
Asp Gly Gly Ser Phe Leu Val Met Val Cys Ala Asn Asp Thr Met Tyr		525
	530	535
Glu Val Leu Val Pro Phe Trp Pro Trp Leu Ala Gly Gln Cys Arg Ile		540
545	550	555
		560

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<210> 101
<211> 456
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(456)
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<400> 101

atg ctg agc agc cag tat ggg ctg atc gtg ttc gtg gcg ggg ctg ctg 48
Met Leu Ser Ser Gln Tyr Gly Leu Ile Val Phe Val Ala Gly Leu Leu
1 5 10 15

ctg ctg ctg gcc tgg gcc gtt cga ccg cgg gca tgc tgt ggt acg tgg 96
Leu Leu Leu Ala Trp Ala Val Arg Pro Arg Ala Cys Cys Gly Thr Trp
20 25 30

gcc gca ctc cgg aac cgc cgc ctc ttc cgc ctc aag gac acg cac gcc 144
Ala Ala Leu Arg Asn Arg Arg Leu Phe Arg Leu Lys Asp Thr His Ala

35	40	45	
ggc gcc ggc tgg ctg cac cgg ctg gag cct cct ctc cgc ctc cag acg			192
Gly Ala Gly Trp Leu His Arg Leu Glu Pro Pro Leu Arg Leu Gln Thr			
50	55	60	
ctt cca tca tta cag cca cag tta cag aaa cct ctc ctg tcc ttc cct			240
Leu Pro Ser Leu Gln Pro Gln Leu Gln Lys Pro Leu Leu Ser Phe Pro			
65	70	75	80
ggc tta aag cca tac agt ggc cct act gac ccc atg agg gag ttc agt			288
Gly Leu Lys Pro Tyr Ser Gly Pro Thr Asp Pro Met Arg Glu Phe Ser			
	85	90	95
tct gtt gct gat gta cta tgg ctg caa gct gcc aaa tgc tgc ttc cct			336
Ser Val Ala Asp Val Leu Trp Leu Gln Ala Ala Lys Cys Cys Phe Pro			
	100	105	110
ctg ctt gtt aaa gag cca agc aac cca tct gat tta ccg agt aga gct			384
Leu Leu Val Lys Glu Pro Ser Asn Pro Ser Asp Leu Pro Ser Arg Ala			
	115	120	125
cgt tca gga cct tca tca aat cat ctt gga gct gct ggc cga ctt ctt			432
Arg Ser Gly Pro Ser Ser Asn His Leu Gly Ala Ala Gly Arg Leu Leu			
	130	135	140
tac tct gca agg aaa gag gaa tga			456
Tyr Ser Ala Arg Lys Glu Glu *			
145	150		

<210> 102

<211> 151

<212> PRT

<213> Homo sapiens

<400> 102

Met Leu Ser Ser Gln Tyr Gly Leu Ile Val Phe Val Ala Gly Leu Leu			
1	5	10	15
Leu Leu Leu Ala Trp Ala Val Arg Pro Arg Ala Cys Cys Gly Thr Trp			
	20	25	30
Ala Ala Leu Arg Asn Arg Arg Leu Phe Arg Leu Lys Asp Thr His Ala			
	35	40	45

Gly Ala Gly Trp Leu His Arg Leu Glu Pro Pro Leu Arg Leu Gln Thr
 50 55 60
 Leu Pro Ser Leu Gln Pro Gln Leu Gln Lys Pro Leu Leu Ser Phe Pro
 65 70 75 80
 Gly Leu Lys Pro Tyr Ser Gly Pro Thr Asp Pro Met Arg Glu Phe Ser
 85 90 95
 Ser Val Ala Asp Val Leu Trp Leu Gln Ala Ala Lys Cys Cys Phe Pro
 100 105 110
 Leu Leu Val Lys Glu Pro Ser Asn Pro Ser Asp Leu Pro Ser Arg Ala
 115 120 125
 Arg Ser Gly Pro Ser Ser Asn His Leu Gly Ala Ala Gly Arg Leu Leu
 130 135 140
 Tyr Ser Ala Arg Lys Glu Glu
 145 150

<210> 103
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(414)

<400> 103

atg ggg cga gtc cgg acc ttg gcg ggc gag tgc tcg gcg cag gcg caa 48
 Met Gly Arg Val Arg Thr Leu Ala Gly Glu Cys Ser Ala Gln Ala Gln
 1 5 10 15

gcg cag agt ctc ctc gcg gtc gtc ctt ttg gcc cct ccc ctc tgg ggg 96
 Ala Gln Ser Leu Leu Ala Val Val Leu Leu Ala Pro Pro Leu Trp Gly
 20 25 30

acc ccc agt gcc agg ctg tca gtg cgc agc ccc cag cct gcg gga ccc 144
 Thr Pro Ser Ala Arg Leu Ser Val Arg Ser Pro Gln Pro Ala Gly Pro
 35 40 45

ctg ggg act ctg ggc gcc tgt tct gca aat gac cgg ttc tta cga gtt 192
 Leu Gly Thr Leu Gly Ala Cys Ser Ala Asn Asp Arg Phe Leu Arg Val
 50 55 60

caa gct gaa cca gcc acc cga gga tgg cat ctc ctc cgt gaa gtt aag 240
 Gln Ala Glu Pro Ala Thr Arg Gly Trp His Leu Leu Arg Glu Val Lys

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<210> 104
<211> 137
<212> PRT
<213> Homo sapiens

      <400> 104
Met Gly Arg Val Arg Thr Leu Ala Gly Glu Cys Ser Ala Gln Ala Gln
 1          5          10          15
Ala Gln Ser Leu Leu Ala Val Val Leu Leu Ala Pro Pro Leu Trp Gly
          20          25          30
Thr Pro Ser Ala Arg Leu Ser Val Arg Ser Pro Gln Pro Ala Gly Pro
          35          40          45
Leu Gly Thr Leu Gly Ala Cys Ser Ala Asn Asp Arg Phe Leu Arg Val
          50          55          60
Gln Ala Glu Pro Ala Thr Arg Gly Trp His Leu Leu Arg Glu Val Lys
65          70          75          80
Pro Pro His Pro Ser Gln Ser Trp Val Val Ser Phe Leu Gly Asp Val
          85          90          95
Pro Cys Val Phe Thr Met Trp Pro Gly Asn Phe Met Ala Val Lys Tyr
          100          105          110
Gln Ala His Arg Gly Pro Ser Trp Glu Trp Ala Phe Leu Ile Ser Ile
          115          120          125
Tyr Pro Leu Gly Arg Arg Val Lys Cys
          130          135

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<210> 105
 <211> 1260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1260)

<400> 105

atg ggg ccc atg ctg ctg cct ctg gct ctg ctg gcc ctg ctg ctg ggg	48
Met Gly Pro Met Leu Leu Pro Leu Ala Leu Leu Ala Leu Leu Leu Gly	
1 5 10 15	
cct gcg ctg gcc cgg agt gcc cgg gac ccg gag gtg ttc tgt gga ggc	96
Pro Ala Leu Ala Arg Ser Ala Arg Asp Pro Glu Val Phe Cys Gly Gly	
20 25 30	
gtc ata tta gca ata aaa tgc atg aaa cca gca ttc ttt gcc acc ttc	144
Val Ile Leu Ala Ile Lys Cys Met Lys Pro Ala Phe Phe Ala Thr Phe	
35 40 45	
tcg cta atc att gct att ttc tcg gag aga gag gct ctt ggc aaa ggt	192
Ser Leu Ile Ile Ala Ile Phe Ser Glu Arg Glu Ala Leu Gly Lys Gly	
50 55 60	
cac agc cct gga ccc ggt ttt cct tcc tgg aat att tgg gtg gtg aca	240
His Ser Pro Gly Pro Gly Phe Pro Ser Trp Asn Ile Trp Val Val Thr	
65 70 75 80	
tcg cag ctg agc ccc ttc cat gga att ctg tgg tgt tgg gct gtt ctt	288
Ser Gln Leu Ser Pro Phe His Gly Ile Leu Trp Cys Trp Ala Val Leu	
85 90 95	
caa gag aag att agg aca cag aca cac aca gag gga cgg cca cgt gag	336
Gln Glu Lys Ile Arg Thr Gln Thr His Thr Glu Gly Arg Pro Arg Glu	
100 105 110	
gac ata ggg aga aga cag ctg tct gca agt caa gga ggg gcc tca gaa	384
Asp Ile Gly Arg Arg Gln Leu Ser Ala Ser Gln Gly Gly Ala Ser Glu	
115 120 125	

gga acc aac cct cct gac acc ttg atc ttg gac ttc cag ctg cag aac 432
 Gly Thr Asn Pro Pro Asp Thr Leu Ile Leu Asp Phe Gln Leu Gln Asn
 130 135 140

ggg tgt ttt ggc aaa tac acc ttc atc tgc tct tca cct ggt aaa tgc 480
 Gly Cys Phe Gly Lys Tyr Thr Phe Ile Cys Ser Ser Pro Gly Lys Cys
 145 150 155 160

ctg atc atc ttt cag gtc cta ctt gtc atg ctc tta ggg aag cct ccc 528
 Leu Ile Ile Phe Gln Val Leu Leu Val Met Leu Leu Gly Lys Pro Pro
 165 170 175

gtg ttc ttt gac aag aag gtc ccg tgc gtg gat caa ggc cct ccc tac 576
 Val Phe Phe Asp Lys Lys Val Pro Ser Val Asp Gln Gly Pro Pro Tyr
 180 185 190

tcc agt atg act tgg tct gaa tca atc cca tct gca aag acc cta ttc 624
 Ser Ser Met Thr Trp Ser Glu Ser Ile Pro Ser Ala Lys Thr Leu Phe
 195 200 205

cca aat aag gcc aca ttc aca gcg tgc agg gcg ctg atg gac gag ata 672
 Pro Asn Lys Ala Thr Phe Thr Ala Cys Arg Ala Leu Met Asp Glu Ile
 210 215 220

gag cac gac atc acc aag gct cgg cag aag aag acc aag gtg gga tcc 720
 Glu His Asp Ile Thr Lys Ala Arg Gln Lys Lys Thr Lys Val Gly Ser
 225 230 235 240

ttc cga atc aat ccc gat ggg act cag gag agg aga aag cac cta aat 768
 Phe Arg Ile Asn Pro Asp Gly Thr Gln Glu Arg Arg Lys His Leu Asn
 245 250 255

ttt gtg tct cgt caa gtc gaa aga cat ttc ggc act gtt ctt cat cag 816
 Phe Val Ser Arg Gln Val Glu Arg His Phe Gly Thr Val Leu His Gln
 260 265 270

aat aaa aat agc gcg tct gtg gtt ctt ggc aca ctc aag gat gga tcc 864
 Asn Lys Asn Ser Ala Ser Val Val Leu Gly Thr Leu Lys Asp Gly Ser
 275 280 285

ttc aag agc cgt gtc tgg caa gtc cac cgg agg gac ccc gtg cag gcc 912
 Phe Lys Ser Arg Val Trp Gln Val His Arg Arg Asp Pro Val Gln Ala
 290 295 300

<210> 106
<211> 419
<212> PRT
<213> Homo sapiens

<400> 106
Met Gly Pro Met Leu Leu Pro Leu Ala Leu Leu Ala Leu Leu Leu Gly
1 5 10 15
Pro Ala Leu Ala Arg Ser Ala Arg Asp Pro Glu Val Phe Cys Gly Gly

Gly Glu Glu Phe Phe Pro His Arg Ser Ser His Ser Asp Pro Glu Thr
 370 375 380
 Ser Ala Ala Ala Ser Val Asn Ala Thr Ser Gln Arg Val Lys Gly Gly
 385 390 395 400
 Ser Leu Arg Lys Tyr Thr Glu Thr Ile Val Thr Val Leu Val Ser Ala
 405 410 415
 Tyr Tyr Cys

<210> 107
 <211> 669
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(669)

<400> 107

atg gcg cct cct ctg cga ccc ctc gcc cgg ctg cga ccg ccg ggg atg 48
 Met Ala Pro Pro Leu Arg Pro Leu Ala Arg Leu Arg Pro Pro Gly Met
 1 5 10 15

ctg ctc cgc gcg ctc ctg ctc ctg ctg ctg ctc agt cct ttg cca ggg 96
 Leu Leu Arg Ala Leu Leu Leu Leu Leu Leu Ser Pro Leu Pro Gly
 20 25 30

ctg cga gag gga ata ggt gaa ctc ata acc cca atc ggc acc agc ttg 144
 Leu Arg Glu Gly Ile Gly Glu Leu Ile Thr Pro Ile Gly Thr Ser Leu
 35 40 45

ccg gat ctg gat cca gcc agg agg aga tgg gag ggt gga att ggc agg 192
 Pro Asp Leu Asp Pro Ala Arg Arg Arg Trp Glu Gly Gly Ile Gly Arg
 50 55 60

gtt gga agt gaa gtg gcc gat ttg tgc ccc gga aag gag ggg gga aaa 240
 Val Gly Ser Glu Val Ala Asp Leu Cys Pro Gly Lys Glu Gly Gly Lys
 65 70 75 80

gtc ccc gaa gct gaa aag gaa gga gtg tgg tgc ttt agc gaa ctg tct 288
 Val Pro Glu Ala Glu Lys Glu Gly Val Trp Cys Phe Ser Glu Leu Ser
 85 90 95

ttt gta aaa gaa cca cag gat gta act gtc aca aga aag gac cca gtc 336
 Phe Val Lys Glu Pro Gln Asp Val Thr Val Thr Arg Lys Asp Pro Val
 100 105 110

gtt tta gat tgc cag gct cac gga gaa gtt cct att aag gtc aca tgg 384
 Val Leu Asp Cys Gln Ala His Gly Glu Val Pro Ile Lys Val Thr Trp
 115 120 125

ttg aaa aat gga gca aaa atg tct gaa aat aaa cgg atc gag gtt ctt 432
 Leu Lys Asn Gly Ala Lys Met Ser Glu Asn Lys Arg Ile Glu Val Leu
 130 135 140

tct aac ggc tct tta tac atc agt gag gtg gaa ggc agg cga gga gag 480
 Ser Asn Gly Ser Leu Tyr Ile Ser Glu Val Glu Gly Arg Arg Gly Glu
 145 150 155 160

cag tcc gat gaa gga ttt tat cag tgc ttg gca atg aac aaa tat gga 528
 Gln Ser Asp Glu Gly Phe Tyr Gln Cys Leu Ala Met Asn Lys Tyr Gly
 165 170 175

gcc att ctt agt caa aaa gct cat ctt gcc tta tca atg tta gcg gca 576
 Ala Ile Leu Ser Gln Lys Ala His Leu Ala Leu Ser Met Leu Ala Ala
 180 185 190

tcc ctg gcc tct acc ctc cca ata ccg ata gac tct ctt cca gtt gtg 624
 Ser Leu Ala Ser Thr Leu Pro Ile Pro Ile Asp Ser Leu Pro Val Val
 195 200 205

aca acc aag aaa gtt cta ctg tgg ggc aaa ata act cct gat tga 669
 Thr Thr Lys Lys Val Leu Leu Trp Gly Lys Ile Thr Pro Asp *
 210 215 220

<210> 108

<211> 222

<212> PRT

<213> Homo sapiens

<400> 108

Met Ala Pro Pro Leu Arg Pro Leu Ala Arg Leu Arg Pro Pro Gly Met
 1 5 10 15

Leu Leu Arg Ala Leu Leu Leu Leu Leu Leu Ser Pro Leu Pro Gly
 20 25 30

Leu Arg Glu Gly Ile Gly Glu Leu Ile Thr Pro Ile Gly Thr Ser Leu
 35 40 45
 Pro Asp Leu Asp Pro Ala Arg Arg Arg Trp Glu Gly Gly Ile Gly Arg
 50 55 60
 Val Gly Ser Glu Val Ala Asp Leu Cys Pro Gly Lys Glu Gly Gly Lys
 65 70 75 80
 Val Pro Glu Ala Glu Lys Glu Gly Val Trp Cys Phe Ser Glu Leu Ser
 85 90 95
 Phe Val Lys Glu Pro Gln Asp Val Thr Val Thr Arg Lys Asp Pro Val
 100 105 110
 Val Leu Asp Cys Gln Ala His Gly Glu Val Pro Ile Lys Val Thr Trp
 115 120 125
 Leu Lys Asn Gly Ala Lys Met Ser Glu Asn Lys Arg Ile Glu Val Leu
 130 135 140
 Ser Asn Gly Ser Leu Tyr Ile Ser Glu Val Glu Gly Arg Arg Gly Glu
 145 150 155 160
 Gln Ser Asp Glu Gly Phe Tyr Gln Cys Leu Ala Met Asn Lys Tyr Gly
 165 170 175
 Ala Ile Leu Ser Gln Lys Ala His Leu Ala Leu Ser Met Leu Ala Ala
 180 185 190
 Ser Leu Ala Ser Thr Leu Pro Ile Pro Ile Asp Ser Leu Pro Val Val
 195 200 205
 Thr Thr Lys Lys Val Leu Leu Trp Gly Lys Ile Thr Pro Asp
 210 215 220

<210> 109
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(864)

<400> 109

atg cgg caa acc cta ccg ctg ctg ctg ctg acg gtg ctg cgc ccc agc
 Met Arg Gln Thr Leu Pro Leu Leu Leu Leu Thr Val Leu Arg Pro Ser
 1 5 10 15

48

tgg gca gac cct ccc cag gag aag gtc ccg ctc ttc cgg gtc act cag
 Trp Ala Asp Pro Pro Gln Glu Lys Val Pro Leu Phe Arg Val Thr Gln
 20 25 30

96

cag ggc ccc tgg ggg agc agt ggc agc aac gcc acc gac tcg ccc tgc 144
 Gln Gly Pro Trp Gly Ser Ser Gly Ser Asn Ala Thr Asp Ser Pro Cys
 35 40 45

gag ggg ctg ccc gcc gcg gat gcg acg gcc ttg acc ctg gcg aac cgc 192
 Glu Gly Leu Pro Ala Ala Asp Ala Thr Ala Leu Thr Leu Ala Asn Arg
 50 55 60

aac ctg gag cgc ctg ccc ggc tgc cta ccg cgc aca ctg cgc agc ctc 240
 Asn Leu Glu Arg Leu Pro Gly Cys Leu Pro Arg Thr Leu Arg Ser Leu
 65 70 75 80

gac gcc agc cac aac ctg ctg cgc gcc ctg agc act tcc gag ctc ggc 288
 Asp Ala Ser His Asn Leu Leu Arg Ala Leu Ser Thr Ser Glu Leu Gly
 85 90 95

cac ctg gag cag ctg cag gtg ctg acc ctg cgc cac aac cgc atc gcc 336
 His Leu Glu Gln Leu Gln Val Leu Thr Leu Arg His Asn Arg Ile Ala
 100 105 110

gcg ctg cgc tgg ggc ccg ggt ggg ccg gcg ggg ctg cac acc ctg gac 384
 Ala Leu Arg Trp Gly Pro Gly Gly Pro Ala Gly Leu His Thr Leu Asp
 115 120 125

ctc agc tac aac cag ctg gcc gct ctg ccg ccg tgc acc ggg ccc gcg 432
 Leu Ser Tyr Asn Gln Leu Ala Ala Leu Pro Pro Cys Thr Gly Pro Ala
 130 135 140

ctg agc agc ctc cgc gcc ctg gcg ctc gcc ggg aat ccg ctg cgg gcg 480
 Leu Ser Ser Leu Arg Ala Leu Ala Leu Ala Gly Asn Pro Leu Arg Ala
 145 150 155 160

ctg cag ccc cgg gcc ttc gcc tgc ttc ccc gcg ctg cag ctc ctc aac 528
 Leu Gln Pro Arg Ala Phe Ala Cys Phe Pro Ala Leu Gln Leu Leu Asn
 165 170 175

ctc tcc tgc acc gcg ctg ggt cgc gga gcc cag ggg ggc atc gcc gag 576
 Leu Ser Cys Thr Ala Leu Gly Arg Gly Ala Gln Gly Gly Ile Ala Glu
 180 185 190

gcg gcg ttc gct gga gag gat ggc gcg ccc ctg gtc acg ctc gaa gtc 624
 Ala Ala Phe Ala Gly Glu Asp Gly Ala Pro Leu Val Thr Leu Glu Val
 195 200 205

tgt ccc tcg ttc caa gcc ttt cct gtg aat gaa ccc gaa aac act cga	192
Cys Pro Ser Phe Gln Ala Phe Pro Val Asn Glu Pro Glu Asn Thr Arg	
50 55 60	
cag gtc gtg aat aat cgt ttt aat gag tgt gca aag cgt gcg acg gga	240
Gln Val Val Asn Asn Arg Phe Asn Glu Cys Ala Lys Arg Ala Thr Gly	
65 70 75 80	
cac act ttc ggt ccc ccg cca gag ctc cgg tgc ccc cga gtg acc gct	288
His Thr Phe Gly Pro Pro Pro Glu Leu Arg Cys Pro Arg Val Thr Ala	
85 90 95	
ttc tgc gat cgc gtc cgc cgg gac ccc gtc cct ctt tcc cct tca gtc	336
Phe Cys Asp Arg Val Arg Arg Asp Pro Val Pro Leu Ser Pro Ser Val	
100 105 110	
ttc agg gag ggg gag gcg ctc cgc att agc ggg gca gtt cag caa ccc	384
Phe Arg Glu Gly Glu Ala Leu Arg Ile Ser Gly Ala Val Gln Gln Pro	
115 120 125	
cga ccc cac ccg cgt ggc tcc agg ccc agg ggt ccg ttc act tcc ccg	432
Arg Pro His Pro Arg Gly Ser Arg Pro Arg Gly Pro Phe Thr Ser Pro	
130 135 140	
tcc ggt ttg ggg gac gcc aat tcg cct aag aaa acc ctg gca gaa gag	480
Ser Gly Leu Gly Asp Ala Asn Ser Pro Lys Lys Thr Leu Ala Glu Glu	
145 150 155 160	
cgc gga ccc ttc act aca aac ctc acg tca ggg tta cag cca cat tta	528
Arg Gly Pro Phe Thr Thr Asn Leu Thr Ser Gly Leu Gln Pro His Leu	
165 170 175	
gga acc tct tcg gaa aag ctg aga aat cac tgt ttt gca aaa agc ctt	576
Gly Thr Ser Ser Glu Lys Leu Arg Asn His Cys Phe Ala Lys Ser Leu	
180 185 190	
ctg tac tgt gat ggg gct ttg tgg tga	603
Leu Tyr Cys Asp Gly Ala Leu Trp *	
195 200	

<211> 200
 <212> PRT
 <213> Homo sapiens

<400> 112

Met Glu Lys Glu Leu Ile Phe Ser Pro Trp Arg Val Phe Leu Lys Leu
 1 . 5 10 15
 Leu Ile Leu Ser Val Ser Ala Val Arg Gly Gly Ala Ala Gln Ser Arg
 20 25 30
 Gly Trp Leu Gln Thr Glu Gly Val Val Asp Ser Val Asp Leu Asn Cys
 35 40 45
 Cys Pro Ser Phe Gln Ala Phe Pro Val Asn Glu Pro Glu Asn Thr Arg
 50 55 60
 Gln Val Val Asn Asn Arg Phe Asn Glu Cys Ala Lys Arg Ala Thr Gly
 65 70 75 80
 His Thr Phe Gly Pro Pro Glu Leu Arg Cys Pro Arg Val Thr Ala
 85 90 95
 Phe Cys Asp Arg Val Arg Arg Asp Pro Val Pro Leu Ser Pro Ser Val
 100 105 110
 Phe Arg Glu Gly Glu Ala Leu Arg Ile Ser Gly Ala Val Gln Gln Pro
 115 120 125
 Arg Pro His Pro Arg Gly Ser Arg Pro Arg Gly Pro Phe Thr Ser Pro
 130 135 140
 Ser Gly Leu Gly Asp Ala Asn Ser Pro Lys Lys Thr Leu Ala Glu Glu
 145 150 155 160
 Arg Gly Pro Phe Thr Thr Asn Leu Thr Ser Gly Leu Gln Pro His Leu
 165 170 175
 Gly Thr Ser Ser Glu Lys Leu Arg Asn His Cys Phe Ala Lys Ser Leu
 180 185 190
 Leu Tyr Cys Asp Gly Ala Leu Trp
 195 200

<210> 113
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(285)

<400> 113

atg gct tca gtg gcc tgg gcc gtc ctc aag gtg ctg ctg ctt ctc ccc

Met Ala Ser Val Ala Trp Ala Val Leu Lys Val Leu Leu Leu Leu Pro
 1 5 10 15

act cag act tgg agc ccc gta gga gca gga aat cca ctt agc tat tcg 96
 Thr Gln Thr Trp Ser Pro Val Gly Ala Gly Asn Pro Leu Ser Tyr Ser
 20 25 30

tct aat cct ttt tca agg ttt tta gct tct ttg cga cgg gtt cga aca 144
 Ser Asn Pro Phe Ser Arg Phe Leu Ala Ser Leu Arg Arg Val Arg Thr
 35 40 45

tcc tcc ttt agc tcg gag aag ttt gtt att acc gat cat ctg aaa cct 192
 Ser Ser Phe Ser Ser Glu Lys Phe Val Ile Thr Asp His Leu Lys Pro
 50 55 60

tct tct ctc aac tcg tca aag tca ttc tcc atc cag ctt tgt tcc gtt 240
 Ser Ser Leu Asn Ser Ser Lys Ser Phe Ser Ile Gln Leu Cys Ser Val
 65 70 75 80

gct ggc gag gcg ttg tgt tcc ttt gga gga gaa gag gcg ctc tga 285
 Ala Gly Glu Ala Leu Cys Ser Phe Gly Gly Glu Glu Ala Leu *
 85 90

<210> 114

<211> 94

<212> PRT

<213> Homo sapiens

<400> 114

Met Ala Ser Val Ala Trp Ala Val Leu Lys Val Leu Leu Leu Leu Pro
 1 5 10 15

Thr Gln Thr Trp Ser Pro Val Gly Ala Gly Asn Pro Leu Ser Tyr Ser
 20 25 30

Ser Asn Pro Phe Ser Arg Phe Leu Ala Ser Leu Arg Arg Val Arg Thr
 35 40 45

Ser Ser Phe Ser Ser Glu Lys Phe Val Ile Thr Asp His Leu Lys Pro
 50 55 60

Ser Ser Leu Asn Ser Ser Lys Ser Phe Ser Ile Gln Leu Cys Ser Val
 65 70 75 80

Ala Gly Glu Ala Leu Cys Ser Phe Gly Gly Glu Glu Ala Leu
 85 90

<210> 115
 <211> 312
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(312)

<400> 115

atg gcc ctg ctc ccc act gtt ttg tgt cta tgg gca cag gca cag gtg	48
Met Ala Leu Leu Pro Thr Val Leu Cys Leu Trp Ala Gln Ala Gln Val	
1 5 10 15	

ggt gtc cag aga cat aat cac atc ttc tgg aat gag aag gag cat ggc	96
Gly Val Gln Arg His Asn His Ile Phe Trp Asn Glu Lys Glu His Gly	
20 25 30	

cat ggg aag agc ggg agg cca gtg cct gct acg ctt aga atg acg aga	144
His Gly Lys Ser Gly Arg Pro Val Pro Ala Thr Leu Arg Met Thr Arg	
35 40 45	

gag aaa cga gag aat gac agt ctt tcc act acc tca gat ttg ttc atg	192
Glu Lys Arg Glu Asn Asp Ser Leu Ser Thr Thr Ser Asp Leu Phe Met	
50 55 60	

aca ctg ccc agt gcc ggt gag atg cac tcc cct gcc agg cgt tgg ccc	240
Thr Leu Pro Ser Ala Gly Glu Met His Ser Pro Ala Arg Arg Trp Pro	
65 70 75 80	

aca gca gca gga ggc ttc att aag cag gac atc tac att ttc gtg ctg	288
Thr Ala Ala Gly Gly Phe Ile Lys Gln Asp Ile Tyr Ile Phe Val Leu	
85 90 95	

ctg gaa cat cct ggg agc tct taa	312
Leu Glu His Pro Gly Ser Ser *	
100	

<210> 116
 <211> 103
 <212> PRT
 <213> Homo sapiens

tcc ctc tct tca att cca tgg tat att ttg tcc ttc agt tct gca gag 240
 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
 65 70 75 80

cct gca atc aaa cat gct aaa gca gag aaa tac aat aag aga cct ata 288
 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
 85 90 95

ctt gac att agc aga gga agt cca gct gtg tac act aat tat gat aaa 336
 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
 100 105 110

cat cca ttc aca atg tct ggg agg aga cta gcc aca gac ctg gaa aga 384
 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
 115 120 125

ggt gaa gaa aaa cga cac cat gaa aaa gga gca aag tga 423
 Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys *
 130 135 140

<210> 118

<211> 140

<212> PRT

<213> Homo sapiens

<400> 118

Met Pro Pro Leu Leu Val Leu Leu Leu Leu Leu Pro Pro Pro Leu Ala
 1 5 10 15
 Pro Pro Leu Phe Ser Gln Cys Gly Gly Ser Gly Cys Ser Arg Gln Pro
 20 25 30
 Thr Ile Pro Ile Ser Asn Met Glu Gly Gln Ile Cys Val Lys Pro Ser
 35 40 45
 Gly Ala Lys Ala Ala Pro Glu Pro Leu Glu Glu Leu Ser Lys Met Arg
 50 55 60
 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
 65 70 75 80
 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
 85 90 95
 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
 100 105 110
 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
 115 120 125

Gly Glu Glu Lys Arg His His Glu Lys Gly Ala Lys
 130 135 140

<210> 119
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(336)

<400> 119

atg gga tgc aga ctg ctg acc ctg ctg tgt ttc cta caa cct gct tcc 48
 Met Gly Cys Arg Leu Leu Thr Leu Leu Cys Phe Leu Gln Pro Ala Ser
 1 5 10 15

agc tcc tcg tgg ctc ttt ggc tcc caa tcc aga gct ttc gcg aac acc 96
 Ser Ser Ser Trp Leu Phe Gly Ser Gln Ser Arg Ala Phe Ala Asn Thr
 20 25 30

aga gcc cct gtg cct ctc cct gca gct ggc tgg gag ttc cag ggc att 144
 Arg Ala Pro Val Pro Leu Pro Ala Ala Gly Trp Glu Phe Gln Gly Ile
 35 40 45

aac aca gac agt ctt tgc cca tca gcc agt gac tgt atg gag ctt gga 192
 Asn Thr Asp Ser Leu Cys Pro Ser Ala Ser Asp Cys Met Glu Leu Gly
 50 55 60

tgt gaa tac aca gct cct gca tcc ctc cga ggc atc tcc aca ccg tct 240
 Cys Glu Tyr Thr Ala Pro Ala Ser Leu Arg Gly Ile Ser Thr Pro Ser
 65 70 75 80

ccc aga gaa tgt ctc gta aaa gct gct cct ctt ggg gag gct ctg ggc 288
 Pro Arg Glu Cys Leu Val Lys Ala Ala Pro Leu Gly Glu Ala Leu Gly
 85 90 95

ttt gga gag agc acc tgg aat tcc cca cta gaa aag ccc aaa aac tga 336
 Phe Gly Glu Ser Thr Trp Asn Ser Pro Leu Glu Lys Pro Lys Asn *
 100 105 110

<210> 120

$\langle 400 \rangle$ 120

<210> 121
<211> 336
<212> DNA
<213> Homo sapiens

<400> 121

atg	aag	ctc	ctt	ctt	ctg	ctt	ttg	act	gtt	act	ctg	ctc	ctg	gcc	cag		48
Met	Lys	Leu	Leu	Leu	Leu	Leu	Leu	Thr	Val	Thr	Leu	Leu	Leu	Ala	Gln		
1				5					10					15			
gtc	acc	cca	ggg	ctg	cca	gcc	atg	aaa	ctt	ctt	tac	ctg	ttt	ctt	gcc		96
Val	Thr	Pro	Gly	Leu	Pro	Ala	Met	Lys	Leu	Leu	Tyr	Leu	Phe	Leu	Ala		
			20					25					30				
atc	ctt	ctg	gcc	ata	gaa	gaa	cca	gtg	ata	tca	gta	gag	tgt	tgg	atg		144
Ile	Leu	Leu	Ala	Ile	Glu	Glu	Pro	Val	Ile	Ser	Val	Glu	Cys	Trp	Met		
		35					40					45					
gat	gga	cac	tgc	cgg	ttg	ttg	tgc	aaa	gat	ggg	gaa	gac	agc	atc	ata		192

Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
 50 55 60

cgc tgc cga aat cgt aaa cgg tgc tgt gtt cct agt cgt tat tta aca 240
 Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
 65 70 75 80

atc caa cca gta aca att cat gga atc ctt ggc tgg acc act cct cag 288
 Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
 85 90 95

atg tcc aca aca gct cca aaa atg aag aca aat ata act aat aga tag 336
 Met Ser Thr Thr Ala Pro Lys Met Lys Thr Asn Ile Thr Asn Arg *
 100 105 110

<210> 122

<211> 111

<212> PRT

<213> Homo sapiens

<400> 122

Met Lys Leu Leu Leu Leu Leu Leu Thr Val Thr Leu Leu Leu Ala Gln
 1 5 10 15
 Val Thr Pro Gly Leu Pro Ala Met Lys Leu Leu Tyr Leu Phe Leu Ala
 20 25 30
 Ile Leu Leu Ala Ile Glu Glu Pro Val Ile Ser Val Glu Cys Trp Met
 35 40 45
 Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
 50 55 60
 Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
 65 70 75 80
 Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
 85 90 95
 Met Ser Thr Thr Ala Pro Lys Met Lys Thr Asn Ile Thr Asn Arg
 100 105 110

<210> 123

<211> 297

<212> DNA

<213> Homo sapiens

<220>

Gly His Ile Arg Pro Leu Gln Ala Pro Ser Gly Pro Thr Asp Arg Thr
 35 40 45
 Leu Asp Gly Arg Ser Gln Asp Val Asn Gly Ile Ser Val Thr Pro Ser
 50 55 60
 Ser Thr Pro Glu Pro Gln Ala Gly Gly Asn Arg Asp Lys Gln Thr Thr
 65 70 75 80
 His Leu Gly Pro Glu Asp Asp Ala Glu Arg Pro Thr Ser Glu Thr Leu
 85 90 95
 Glu Glu

<210> 125
 <211> 630
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(630)

<400> 125
 atg aga tcc ggg agg cac ccc tcg ctg ctg ctg ctt cta gtg ctg ctg 48
 Met Arg Ser Gly Arg His Pro Ser Leu Leu Leu Leu Val Leu Leu
 1 5 10 15

 ctg tgg ctg ctg cag aca ctg ctc act aga tta ggg ccc act cta acc 96
 Leu Trp Leu Leu Gln Thr Leu Leu Thr Arg Leu Gly Pro Thr Leu Thr
 20 25 30

 cag tgt gac ttc atc tta act gta att cag tta aga att aca tct gca 144
 Gln Cys Asp Phe Ile Leu Thr Val Ile Gln Leu Arg Ile Thr Ser Ala
 35 40 45

 aat agc cta ttt cca aat aag gtc ccg ttc aca ggt aaa ccc aac ggg 192
 Asn Ser Leu Phe Pro Asn Lys Val Pro Phe Thr Gly Lys Pro Asn Gly
 50 55 60

 gtc cat gcg cag tcc tat acg atc tta gta ctc ctc atc gcg tcc cga 240
 Val His Ala Gln Ser Tyr Thr Ile Leu Val Leu Leu Ile Ala Ser Arg
 65 70 75 80

 ggt aat gtt tgc agc tgc gta gag tct atc ttt ata ggc cgg ccg atg 288
 Gly Asn Val Cys Ser Cys Val Glu Ser Ile Phe Ile Gly Arg Pro Met

	85	90	95	
gtt gcg ggt gcc cct cgt cgc ggg tgc gcg cac agg gca acc aga att				336
Val Ala Gly Ala Pro Arg Arg Gly Cys Ala His Arg Ala Thr Arg Ile				
	100	105	110	
aaa acc act att att agg cga aac aag acg ctg gag gtg gta ggc ctc				384
Lys Thr Thr Ile Ile Arg Arg Asn Lys Thr Leu Glu Val Val Gly Leu				
	115	120	125	
aaa ctg ttt ctg ctc gtg tgc acg gcg gac tca gtt ccc cgg aat gtt				432
Lys Leu Phe Leu Leu Val Ser Thr Ala Asp Ser Val Pro Arg Asn Val				
	130	135	140	
cgg gct gtg tgc gag gaa gac gcg gag gaa tca tct gca ggc agt ctc				480
Arg Ala Val Ser Glu Glu Asp Ala Glu Glu Ser Ser Ala Gly Ser Leu				
	145	150	155	160
gtc cac gta ttt caa aaa ttt gcg aat ata ccc gtc gtg ggg aaa tac				528
Val His Val Phe Gln Lys Phe Ala Asn Ile Pro Val Val Gly Lys Tyr				
	165	170	175	
ccg tgc tat ttt ggg gag gct ttg ccc aga ctt tct cga ttg gat tac				576
Pro Cys Tyr Phe Gly Glu Ala Leu Pro Arg Leu Ser Arg Leu Asp Tyr				
	180	185	190	
aga atc tac cgt tac tgc tgc gga tgc cag agg ttg cga tgc tgt gga				624
Arg Ile Tyr Arg Tyr Cys Ser Gly Cys Gln Arg Leu Arg Cys Cys Gly				
	195	200	205	
gag tga				630
Glu *				

<210> 126

<211> 209

<212> PRT

<213> Homo sapiens

<400> 126

Met	Arg	Ser	Gly	Arg	His	Pro	Ser	Leu	Leu	Leu	Leu	Val	Leu	Leu
1				5				10				15		

Leu Trp Leu Leu Gln Thr Leu Leu Thr Arg Leu Gly Pro Thr Leu Thr
 20 25 30
 Gln Cys Asp Phe Ile Leu Thr Val Ile Gln Leu Arg Ile Thr Ser Ala
 35 40 45
 Asn Ser Leu Phe Pro Asn Lys Val Pro Phe Thr Gly Lys Pro Asn Gly
 50 55 60
 Val His Ala Gln Ser Tyr Thr Ile Leu Val Leu Leu Ile Ala Ser Arg
 65 70 75 80
 Gly Asn Val Cys Ser Cys Val Glu Ser Ile Phe Ile Gly Arg Pro Met
 85 90 95
 Val Ala Gly Ala Pro Arg Arg Gly Cys Ala His Arg Ala Thr Arg Ile
 100 105 110
 Lys Thr Thr Ile Ile Arg Arg Asn Lys Thr Leu Glu Val Val Gly Leu
 115 120 125
 Lys Leu Phe Leu Leu Val Ser Thr Ala Asp Ser Val Pro Arg Asn Val
 130 135 140
 Arg Ala Val Ser Glu Glu Asp Ala Glu Glu Ser Ser Ala Gly Ser Leu
 145 150 155 160
 Val His Val Phe Gln Lys Phe Ala Asn Ile Pro Val Val Gly Lys Tyr
 165 170 175
 Pro Cys Tyr Phe Gly Glu Ala Leu Pro Arg Leu Ser Arg Leu Asp Tyr
 180 185 190
 Arg Ile Tyr Arg Tyr Cys Ser Gly Cys Gln Arg Leu Arg Cys Cys Gly
 195 200 205
 Glu

<210> 127
 <211> 348
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(348)

<400> 127

atg ggg ccc ctt atc tcc ccc ggc act ttc ccc tac atc cgg ctg caa 48
 Met Gly Pro Leu Ile Ser Pro Gly Thr Phe Pro Tyr Ile Arg Leu Gln
 1 5 10 15

cta gaa gct ttc gca cta acc ctc gtg gct gcc cca cgc tgg gcc ctg 96
 Leu Glu Ala Phe Ala Leu Thr Leu Val Ala Ala Pro Arg Trp Ala Leu

	20	25	30	
gcc ttt gta aac ggt tcc ttt att aaa ctc tct cca aat acc cac ggc				144
Ala Phe Val Asn Gly Ser Phe Ile Lys Leu Ser Pro Asn Thr His Gly				
	35	40	45	
atg cgt gtg aca gcg gac tcc ttc ctg ccc gtc aca ccg gcg atg tgc				192
Met Arg Val Thr Ala Asp Ser Phe Leu Pro Val Thr Pro Ala Met Cys				
	50	55	60	
aca aaa agt atc tca gac cct ctc ctc acc cca cct gat ccc gtc aaa				240
Thr Lys Ser Ile Ser Asp Pro Leu Leu Thr Pro Pro Asp Pro Val Lys				
	65	70	75	80
aag gcc tcc atg aac gcc acc ctc cat gct ggg gtc tcg ggg cct gca				288
Lys Ala Ser Met Asn Ala Thr Leu His Ala Gly Val Ser Gly Pro Ala				
	85	90	95	
aga tcc cag ctc agt gga ttt gaa gga act gat ggg cct gga gtc tgg				336
Arg Ser Gln Leu Ser Gly Phe Glu Gly Thr Asp Gly Pro Gly Val Trp				
	100	105	110	
cag tgt gaa tga				348
Gln Cys Glu *				
	115			

<210> 128

<211> 115

<212> PRT

<213> Homo sapiens

<400> 128

Met Gly Pro Leu Ile Ser Pro Gly Thr Phe Pro Tyr Ile Arg Leu Gln				
1	5	10	15	
Leu Glu Ala Phe Ala Leu Thr Leu Val Ala Ala Pro Arg Trp Ala Leu				
	20	25	30	
Ala Phe Val Asn Gly Ser Phe Ile Lys Leu Ser Pro Asn Thr His Gly				
	35	40	45	
Met Arg Val Thr Ala Asp Ser Phe Leu Pro Val Thr Pro Ala Met Cys				
	50	55	60	
Thr Lys Ser Ile Ser Asp Pro Leu Leu Thr Pro Pro Asp Pro Val Lys				
	65	70	75	80

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<210> 129
<211> 660
<212> DNA
<213> Homo sapiens
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<400> 129

ctg atg gca tta ccc ctt cca gct gcc tct ctc cag aat gat ctc aac 96
Leu Met Ala Leu Pro Leu Pro Ala Ala Ser Leu Gln Asn Asp Leu Asn
20 25 30

cag ggt ggc cca ggg agc act aat tcc aag agg cag gcc aac tgg tcc 144
Gln Gly Gly Pro Gly Ser Thr Asn Ser Lys Arg Gln Ala Asn Trp Ser
35 40 45

ttg gag gag gag aag agc aga ctg ctg gct gag gca gca ctt gag ttg 192
Leu Glu Glu Glu Lys Ser Arg Leu Leu Ala Glu Ala Ala Leu Glu Leu
50 55 60

cgg gag gag aac acg agg cag gaa cgg att ctg gcc ctg gcc aag cga 240
Arg Glu Glu Asn Thr Arg Gln Glu Arg Ile Leu Ala Leu Ala Lys Arg
65 70 75 80

cta gcc atg ctg cgg gga cag gac ccc gag aga gtg acc ctc cag gac 288
Leu Ala Met Leu Arg Gly Gln Asp Pro Glu Arg Val Thr Leu Gln Asp
85 90 95

tat cgc ctc cca gac agt gat gac gac gag gat gag gag aca gcc atc 336
Tyr Arg Leu Pro Asp Ser Asp Asp Asp Glu Asp Glu Glu Thr Ala Ile

100	105	110	
caa aga gtc ctg cag cag ctc act gaa gaa gct tcc ctg gat gag gca			384
Gln Arg Val Leu Gln Gln Leu Thr Glu Glu Ala Ser Leu Asp Glu Ala			
115	120	125	
agt ggc ttt aac atc cct gca gag cag gct tct cga ccc tgg acg caa			432
Ser Gly Phe Asn Ile Pro Ala Glu Gln Ala Ser Arg Pro Trp Thr Gln			
130	135	140	
ccc cgc ggg gca gag cct gag gcc cag gat gtg gac ccc agg cct gag			480
Pro Arg Gly Ala Glu Pro Glu Ala Gln Asp Val Asp Pro Arg Pro Glu			
145	150	155	160
gct gag gaa gag gag ctc ccc tgg tgc tgc atc tgc aat gag gat gcc			528
Ala Glu Glu Glu Glu Leu Pro Trp Cys Cys Ile Cys Asn Glu Asp Ala			
165	170	175	
acc cta cgc tgc gct ggc tgc gat ggg gac ctc ttc tgt gcc cgc tgc			576
Thr Leu Arg Cys Ala Gly Cys Asp Gly Asp Leu Phe Cys Ala Arg Cys			
180	185	190	
ttc cga gag ggc cat gat gcc ttt gag ctt aaa gag cac cag aca tct			624
Phe Arg Glu Gly His Asp Ala Phe Glu Leu Lys Glu His Gln Thr Ser			
195	200	205	
gcc tac tct cct cca cgt gca ggc caa gag cac tga			660
Ala Tyr Ser Pro Pro Arg Ala Gly Gln Glu His *			
210	215		

<210> 130

<211> 219

<212> PRT

<213> Homo sapiens

<400> 130

Met Gly Ser Leu Ala Ser Glu Glu Arg Tyr Trp Asp Val Ser Ala Leu	
1 5 10 15	
Leu Met Ala Leu Pro Leu Pro Ala Ala Ser Leu Gln Asn Asp Leu Asn	
20 25 30	
Gln Gly Gly Pro Gly Ser Thr Asn Ser Lys Arg Gln Ala Asn Trp Ser	
35 40 45	

Leu Glu Glu Glu Lys Ser Arg Leu Leu Ala Glu Ala Ala Leu Glu Leu
 50 55 60
 Arg Glu Glu Asn Thr Arg Gln Glu Arg Ile Leu Ala Leu Ala Lys Arg
 65 70 75 80
 Leu Ala Met Leu Arg Gly Gln Asp Pro Glu Arg Val Thr Leu Gln Asp
 85 90 95
 Tyr Arg Leu Pro Asp Ser Asp Asp Glu Asp Glu Glu Thr Ala Ile
 100 105 110
 Gln Arg Val Leu Gln Gln Leu Thr Glu Glu Ala Ser Leu Asp Glu Ala
 115 120 125
 Ser Gly Phe Asn Ile Pro Ala Glu Gln Ala Ser Arg Pro Trp Thr Gln
 130 135 140
 Pro Arg Gly Ala Glu Pro Glu Ala Gln Asp Val Asp Pro Arg Pro Glu
 145 150 155 160
 Ala Glu Glu Glu Glu Leu Pro Trp Cys Cys Ile Cys Asn Glu Asp Ala
 165 170 175
 Thr Leu Arg Cys Ala Gly Cys Asp Gly Asp Leu Phe Cys Ala Arg Cys
 180 185 190
 Phe Arg Glu Gly His Asp Ala Phe Glu Leu Lys Glu His Gln Thr Ser
 195 200 205
 Ala Tyr Ser Pro Pro Arg Ala Gly Gln Glu His
 210 215

<210> 131
 <211> 252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(252)

<400> 131

atg cag tgg ctt gct ctg ctt ctc cca cat gca ggc cta gcc cag gca 48
 Met Gln Trp Leu Ala Leu Leu Leu Pro His Ala Gly Leu Ala Gln Ala
 1 5 10 15

atg ctg ctg ggc agg tca gag acc tcc aca cct gtc ctc ttc gcg tgc 96
 Met Leu Leu Gly Arg Ser Glu Thr Ser Thr Pro Val Leu Phe Ala Cys
 20 25 30

cac atg gac acg ggc ctg cgc agc gtg gcc aac atc tgg ttc caa tgt 144
 His Met Asp Thr Gly Leu Arg Ser Val Ala Asn Ile Trp Phe Gln Cys

35

40

45

gtg gtt ccc atg cca ctg gct gac tac ccc aat gat gac atg gcc cac 192
 Val Val Pro Met Pro Leu Ala Asp Tyr Pro Asn Asp Asp Met Ala His
 50 55 60

gtt gtc ccc acg gag tcg ctg ctg ctc tca gcc acc gtc acg cgg aga 240
 Val Val Pro Thr Glu Ser Leu Leu Leu Ser Ala Thr Val Thr Arg Arg
 65 70 75 80

gac agg tcc tga 252
 Asp Arg Ser *

<210> 132
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Gln Trp Leu Ala Leu Leu Leu Pro His Ala Gly Leu Ala Gln Ala
 1 5 10 15
 Met Leu Leu Gly Arg Ser Glu Thr Ser Thr Pro Val Leu Phe Ala Cys
 20 25 30
 His Met Asp Thr Gly Leu Arg Ser Val Ala Asn Ile Trp Phe Gln Cys
 35 40 45
 Val Val Pro Met Pro Leu Ala Asp Tyr Pro Asn Asp Asp Met Ala His
 50 55 60
 Val Val Pro Thr Glu Ser Leu Leu Leu Ser Ala Thr Val Thr Arg Arg
 65 70 75 80
 Asp Arg Ser

<210> 133
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(378)

<400> 133

atg	gca	aaa	ata	ggc	gag	gag	agc	tta	aat	tgt	act	ccg	agc	gac	gcg	48
Met	Ala	Lys	Ile	Gly	Glu	Glu	Ser	Leu	Asn	Cys	Thr	Pro	Ser	Asp	Ala	
1				5				10						15		

ctc	cag	tac	aag	gga	atg	ttt	ctt	atg	tat	ctc	ctt	cca	gga	gtg	ttt	96
Leu	Gln	Tyr	Lys	Gly	Met	Phe	Leu	Met	Tyr	Leu	Leu	Pro	Gly	Val	Phe	
			20				25						30			

ggg	cag	gtc	agg	tgc	cca	att	cca	ccc	cag	gac	agt	aag	aga	aag	gtg	144
Gly	Gln	Val	Arg	Cys	Pro	Ile	Pro	Pro	Gln	Asp	Ser	Lys	Arg	Lys	Val	
		35				40						45				

cgg	agc	aag	cac	ccg	gct	cgc	aag	atc	agc	cgc	cgg	gat	aca	aga	acc	192
Arg	Ser	Lys	His	Pro	Ala	Arg	Lys	Ile	Ser	Arg	Arg	Asp	Thr	Arg	Thr	
	50					55					60					

cac	cga	ctg	ctg	ctc	aac	cgc	gca	agt	ccc	tgg	cct	ata	agc	cca	cac	240
His	Arg	Leu	Leu	Leu	Asn	Arg	Ala	Ser	Pro	Trp	Pro	Ile	Ser	Pro	His	
65					70					75					80	

gcc	gaa	aca	aac	agg	aag	gcg	gcc	ctg	gca	cag	atc	gct	cac	tac	cca	288
Ala	Glu	Thr	Asn	Arg	Lys	Ala	Ala	Leu	Ala	Gln	Ile	Ala	His	Tyr	Pro	
				85				90						95		

aaa	ccc	ccg	acc	agc	tgg	aac	gcc	gag	gcc	gac	gac	aac	agt	caa	ggc	336
Lys	Pro	Pro	Thr	Ser	Trp	Asn	Ala	Glu	Ala	Asp	Asp	Asn	Ser	Gln	Gly	
			100				105						110			

aca	aga	ata	cga	gac	cag	gcc	gcg	cca	cac	agg	ctg	ttc	tag			378
Thr	Arg	Ile	Arg	Asp	Gln	Ala	Ala	Pro	His	Arg	Leu	Phe	*			
		115				120						125				

<210> 134

<211> 125

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Lys	Ile	Gly	Glu	Glu	Ser	Leu	Asn	Cys	Thr	Pro	Ser	Asp	Ala
1				5				10						15	
Leu	Gln	Tyr	Lys	Gly	Met	Phe	Leu	Met	Tyr	Leu	Leu	Pro	Gly	Val	Phe

20 25 30
 Gly Gln Val Arg Cys Pro Ile Pro Pro Gln Asp Ser Lys Arg Lys Val
 35 40 45
 Arg Ser Lys His Pro Ala Arg Lys Ile Ser Arg Arg Asp Thr Arg Thr
 50 55 60
 His Arg Leu Leu Leu Asn Arg Ala Ser Pro Trp Pro Ile Ser Pro His
 65 70 75 80
 Ala Glu Thr Asn Arg Lys Ala Ala Leu Ala Gln Ile Ala His Tyr Pro
 85 90 95
 Lys Pro Pro Thr Ser Trp Asn Ala Glu Ala Asp Asp Asn Ser Gln Gly
 100 105 110
 Thr Arg Ile Arg Asp Gln Ala Ala Pro His Arg Leu Phe
 115 120 125

<210> 135
 <211> 87
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(87)

<400> 135
 atg agc tgg cca cac aaa ctg ctg ctg ctg ctg ctt cta ggt ggc tgc 48
 Met Ser Trp Pro His Lys Leu Leu Leu Leu Leu Leu Gly Gly Cys
 1 5 10 15
 ctt gct ggt ata ctt act ccc tac ttc atg aac tca tga 87
 Leu Ala Gly Ile Leu Thr Pro Tyr Phe Met Asn Ser *
 20 25

<210> 136
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Ser Trp Pro His Lys Leu Leu Leu Leu Leu Leu Gly Gly Cys
 1 5 10 15
 Leu Ala Gly Ile Leu Thr Pro Tyr Phe Met Asn Ser
 20 25

<210> 137
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(558)

<400> 137

atg ggg ctt gat gaa cag ctt ttt ggg gca cta gaa gcc tcc tgg ggt	48
Met Gly Leu Asp Glu Gln Leu Phe Gly Ala Leu Glu Ala Ser Trp Gly	
1 5 10 15	
acc tgt cat gcc ctt gaa cgt ttc ttg gag cgt gcc ttt ttc cac cct	96
Thr Cys His Ala Leu Glu Arg Phe Leu Glu Arg Ala Phe Phe His Pro	
20 25 30	
gcc atg aag ccc gaa gtt ctt cta ttg gca acc aaa ttt cca ctg tcc	144
Ala Met Lys Pro Glu Val Leu Leu Ala Thr Lys Phe Pro Leu Ser	
35 40 45	
ctg ggc aaa aga aaa ggg ccc tca tgt gcg ctt aga aga tct ggc gag	192
Leu Gly Lys Arg Lys Gly Pro Ser Cys Ala Leu Arg Arg Ser Gly Glu	
50 55 60	
gac gaa att tat cat gta acc aga aac cta cag aat ttg ctt ttc ata	240
Asp Glu Ile Tyr His Val Thr Arg Asn Leu Gln Asn Leu Leu Phe Ile	
65 70 75 80	
gga aag tca gcc aaa aat atc aac agc cac aat tta tca gac gcc ttc	288
Gly Lys Ser Ala Lys Asn Ile Asn Ser His Asn Leu Ser Asp Ala Phe	
85 90 95	
agg aaa aat gtc aaa gcc agg cat ttg tct gaa gtg acc tat cct gct	336
Arg Lys Asn Val Lys Ala Arg His Leu Ser Glu Val Thr Tyr Pro Ala	
100 105 110	
tca gaa gtc tat cag cca ttt cca ttc ctg ctt ctg aat gga atc aat	384
Ser Glu Val Tyr Gln Pro Phe Pro Phe Leu Leu Leu Asn Gly Ile Asn	
115 120 125	

Met	Gly	Leu	Asp	Glu	Gln	Leu	Phe	Gly	Ala	Leu	Glu	Ala	Ser	Trp	Gly
1				5				10					15		
Thr	Cys	His	Ala	Leu	Glu	Arg	Phe	Leu	Glu	Arg	Ala	Phe	Phe	His	Pro
			20					25					30		
Ala	Met	Lys	Pro	Glu	Val	Leu	Leu	Leu	Ala	Thr	Lys	Phe	Pro	Leu	Ser
		35					40					45			
Leu	Gly	Lys	Arg	Lys	Gly	Pro	Ser	Cys	Ala	Leu	Arg	Arg	Ser	Gly	Glu
50						55					60				
Asp	Glu	Ile	Tyr	His	Val	Thr	Arg	Asn	Leu	Gln	Asn	Leu	Leu	Phe	Ile
65					70					75					80
Gly	Lys	Ser	Ala	Lys	Asn	Ile	Asn	Ser	His	Asn	Leu	Ser	Asp	Ala	Phe
			85					90					95		
Arg	Lys	Asn	Val	Lys	Ala	Arg	His	Leu	Ser	Glu	Val	Thr	Tyr	Pro	Ala
			100					105					110		
Ser	Glu	Val	Tyr	Gln	Pro	Phe	Pro	Phe	Leu	Leu	Leu	Asn	Gly	Ile	Asn
		115					120					125			
Gln	Lys	His	Phe	Gln	Pro	Pro	Leu	Leu	Val	Thr	Asp	Gln	Asn	Ser	Cys
130						135				140					
Gly	Leu	Arg	Val	Ala	Leu	Pro	Pro	Pro	Ala	Pro	Thr	Ser	Ser	Arg	Asn
145					150					155					160

Pro Pro Asp Ala Leu Arg Leu Leu Ser Gln Lys His Asn Gln Asn Asn
 165 170 175

Pro Asn Gly Ile Thr Ile Asn Ile Gln
 180 185

<210> 139

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(303)

<400> 139

atg acc aga gca cct ctc ctg cta cta tgt gtt gcc ctg gtg ctg ctt 48
 Met Thr Arg Ala Pro Leu Leu Leu Leu Cys Val Ala Leu Val Leu Leu
 1 5 10 15

ggg cat gtg aat gga gcc aca gta aga aat gag gac aaa tgg aag cca 96
 Gly His Val Asn Gly Ala Thr Val Arg Asn Glu Asp Lys Trp Lys Pro
 20 25 30

ctc aac aac ccc aga aac aga gat ctg ttt ttc aga agg ctt cag gca 144
 Leu Asn Asn Pro Arg Asn Arg Asp Leu Phe Phe Arg Arg Leu Gln Ala
 35 40 45

tat ttt aag ggc aga ggt ctt gat ctt gga aca ttt cca aat cct ttc 192
 Tyr Phe Lys Gly Arg Gly Leu Asp Leu Gly Thr Phe Pro Asn Pro Phe
 50 55 60

ccc acg aat gaa aat cct aga cct ctc tct ttc cag tca gaa ctt act 240
 Pro Thr Asn Glu Asn Pro Arg Pro Leu Ser Phe Gln Ser Glu Leu Thr
 65 70 75 80

gct tct gca tct gca gat tat gaa gag cag aaa aac tcc ttt cac aat 288
 Ala Ser Ala Ser Ala Asp Tyr Glu Glu Gln Lys Asn Ser Phe His Asn
 85 90 95

tat ctc aaa ggc tga 303
 Tyr Leu Lys Gly *
 100

<210> 140
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 140
 Met Thr Arg Ala Pro Leu Leu Leu Leu Cys Val Ala Leu Val Leu Leu
 1 5 10 15
 Gly His Val Asn Gly Ala Thr Val Arg Asn Glu Asp Lys Trp Lys Pro
 20 25 30
 Leu Asn Asn Pro Arg Asn Arg Asp Leu Phe Phe Arg Arg Leu Gln Ala
 35 40 45
 Tyr Phe Lys Gly Arg Gly Leu Asp Leu Gly Thr Phe Pro Asn Pro Phe
 50 55 60
 Pro Thr Asn Glu Asn Pro Arg Pro Leu Ser Phe Gln Ser Glu Leu Thr
 65 70 75 80
 Ala Ser Ala Ser Ala Asp Tyr Glu Glu Gln Lys Asn Ser Phe His Asn
 85 90 95
 Tyr Leu Lys Gly
 100

<210> 141
 <211> 687
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(687)

<400> 141
 atg cgg ccc ctt aag ccc ggc gcc cct ttg ccc gca ctc ttc ctg ctg 48
 Met Arg Pro Leu Lys Pro Gly Ala Pro Leu Pro Ala Leu Phe Leu Leu
 1 5 10 15
 gcg ctg gct ttg tcc ccg cac gga gcc cac ggg agg ccc cgg ggg cgc 96
 Ala Leu Ala Leu Ser Pro His Gly Ala His Gly Arg Pro Arg Gly Arg
 20 25 30
 agg gga gcg cgc gtc acg gat aag gag ccc aag ccg ttg ctt ttc ctc 144
 Arg Gly Ala Arg Val Thr Asp Lys Glu Pro Lys Pro Leu Leu Phe Leu
 35 40 45

ccc gcg gcc ggg gcc ggc cgg act ccc agc ggc tcc cgg agc gca gga	192
Pro Ala Ala Gly Ala Gly Arg Thr Pro Ser Gly Ser Arg Ser Ala Gly	
50 55 60	
gct ggg cga ggc act cgc ttt ggg aag cct gag att agt aca gca gaa	240
Ala Gly Arg Gly Thr Arg Phe Gly Lys Pro Glu Ile Ser Thr Ala Glu	
65 70 75 80	
aac aga gca tct ctg cag att ccc agc tct cgg aaa gag gtc agg gtc	288
Asn Arg Ala Ser Leu Gln Ile Pro Ser Ser Arg Lys Glu Val Arg Val	
85 90 95	
atg aga cat cca cag gca gag aag tcg tgt gaa tac ggg gaa cac gga	336
Met Arg His Pro Gln Ala Glu Lys Ser Cys Glu Tyr Gly Glu His Gly	
100 105 110	
aaa gcc ccg gaa aag gag gtc cga ggg ggc ggc ccg ggc act tgg ggc	384
Lys Ala Pro Glu Lys Glu Val Arg Gly Gly Gly Pro Gly Thr Trp Gly	
115 120 125	
agc gct gga ggg agg agg gca gga cac gca gga aag gaa ggt ggg gac	432
Ser Ala Gly Gly Arg Arg Ala Gly His Ala Gly Lys Glu Gly Gly Asp	
130 135 140	
aga agc gag aag ctc ctc aca cgt ttc tgt tca cac cca gca aga gca	480
Arg Ser Glu Lys Leu Leu Thr Arg Phe Cys Ser His Pro Ala Arg Ala	
145 150 155 160	
gag caa ggt gaa gct gcc ggc gag gct ggg aca gaa ggg ccc ctc tgc	528
Glu Gln Gly Glu Ala Ala Gly Glu Ala Gly Thr Glu Gly Pro Leu Cys	
165 170 175	
ggg gac att tgg tgg cct cca ccg ggc ttg gga aga gga gag ggc cta	576
Gly Asp Ile Trp Trp Pro Pro Pro Gly Leu Gly Arg Gly Glu Gly Leu	
180 185 190	
ggg tgg cct ggg gat gcc tcg cag cta gcg gct ggc cgt ggg acc aca	624
Gly Trp Pro Gly Asp Ala Ser Gln Leu Ala Ala Gly Arg Gly Thr Thr	
195 200 205	
gct cct gat ccc ttc tcc tca ggc ttt atg gct aag aaa gca aac aag	672
Ala Pro Asp Pro Phe Ser Ser Gly Phe Met Ala Lys Lys Ala Asn Lys	

210

215

220

ggc ttc tta gta tga

Gly Phe Leu Val *

225

687

<210> 142

<211> 228

<212> PRT

<213> Homo sapiens

<400> 142

Met Arg Pro Leu Lys Pro Gly Ala Pro Leu Pro Ala Leu Phe Leu Leu
 1 5 10 15
 Ala Leu Ala Leu Ser Pro His Gly Ala His Gly Arg Pro Arg Gly Arg
 20 25 30
 Arg Gly Ala Arg Val Thr Asp Lys Glu Pro Lys Pro Leu Leu Phe Leu
 35 40 45
 Pro Ala Ala Gly Ala Gly Arg Thr Pro Ser Gly Ser Arg Ser Ala Gly
 50 55 60
 Ala Gly Arg Gly Thr Arg Phe Gly Lys Pro Glu Ile Ser Thr Ala Glu
 65 70 75 80
 Asn Arg Ala Ser Leu Gln Ile Pro Ser Ser Arg Lys Glu Val Arg Val
 85 90 95
 Met Arg His Pro Gln Ala Glu Lys Ser Cys Glu Tyr Gly Glu His Gly
 100 105 110
 Lys Ala Pro Glu Lys Glu Val Arg Gly Gly Gly Pro Gly Thr Trp Gly
 115 120 125
 Ser Ala Gly Gly Arg Arg Ala Gly His Ala Gly Lys Glu Gly Gly Asp
 130 135 140
 Arg Ser Glu Lys Leu Leu Thr Arg Phe Cys Ser His Pro Ala Arg Ala
 145 150 155 160
 Glu Gln Gly Glu Ala Ala Gly Glu Ala Gly Thr Glu Gly Pro Leu Cys
 165 170 175
 Gly Asp Ile Trp Trp Pro Pro Pro Gly Leu Gly Arg Gly Glu Gly Leu
 180 185 190
 Gly Trp Pro Gly Asp Ala Ser Gln Leu Ala Ala Gly Arg Gly Thr Thr
 195 200 205
 Ala Pro Asp Pro Phe Ser Ser Gly Phe Met Ala Lys Lys Ala Asn Lys
 210 215 220
 Gly Phe Leu Val
 225

13330"446600

<210> 143
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(393)

<400> 143

atg	ggg	ttt	ctc	cat	gtt	gag	gct	ggt	ctc	gta	ctc	ctg	acc	tca	ggc	48
Met	Gly	Phe	Leu	His	Val	Glu	Ala	Gly	Leu	Val	Leu	Leu	Thr	Ser	Gly	
1				5					10					15		

gtg	gtc	ccg	ctc	gca	cga	ggg	agc	ggt	cgc	cca	ggg	tgc	cgg	gaa	gtc	96
Val	Val	Pro	Leu	Ala	Arg	Gly	Ser	Gly	Arg	Pro	Gly	Cys	Arg	Glu	Val	
			20					25					30			

ggg	gac	cgg	cca	gcc	gcc	gac	cgg	ccg	cac	ccc	tcc	ccg	ccg	agc	tcg	144
Gly	Asp	Arg	Pro	Ala	Ala	Asp	Arg	Pro	His	Pro	Ser	Pro	Pro	Ser	Ser	
		35					40					45				

cgc	gcc	cgc	ctc	gtc	agc	acc	ttt	ccc	gca	gcg	cag	ccc	cac	agt	ggt	192
Arg	Ala	Arg	Leu	Val	Ser	Thr	Phe	Pro	Ala	Ala	Gln	Pro	His	Ser	Gly	
	50					55					60					

cac	gag	agc	cgc	ggc	ccg	aaa	aga	cgc	gaa	ggt	ggt	gac	gtg	tcc	cgt	240
His	Glu	Ser	Arg	Gly	Pro	Lys	Arg	Arg	Glu	Gly	Gly	Asp	Val	Ser	Arg	
65					70				75						80	

gcc	cag	ggc	gct	gcg	cag	gag	gca	ttg	gca	act	gac	gtc	ctg	cgc	gcc	288
Ala	Gln	Gly	Ala	Ala	Gln	Glu	Ala	Leu	Ala	Thr	Asp	Val	Leu	Arg	Ala	
			85					90					95			

gcc	tgg	tgg	aag	caa	agc	agc	cga	gcc	ccc	cgg	aag	cgg	cgg	cgc	ggg	336
Ala	Trp	Trp	Lys	Gln	Ser	Ser	Arg	Ala	Pro	Arg	Lys	Arg	Arg	Arg	Gly	
			100					105					110			

cga	gtg	gag	aac	gtg	act	tac	gtc	atc	tgg	cgg	agg	cgt	ggg	ggc	ggt	384
Arg	Val	Glu	Asn	Val	Thr	Tyr	Val	Ile	Trp	Arg	Arg	Arg	Gly	Gly	Gly	
		115					120					125				

393

<210> 144
<211> 130
<212> PRT
<213> Homo sapiens

<400> 144

[illegible]

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<210> 145
<211> 666
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(666)
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<400> 145

atg gat acc agc acc tgc tct ggt gga agt ggg agg gga gta aag tgg
Met Asp Thr Ser Thr Cys Ser Gly Gly Ser Gly Arg Gly Val Lys Trp
1 5 10 15

act ctg cgg gag tcc ttg gtt tta gtt ttg ttt agt gca ctg gtt ttc	96
Thr Leu Arg Glu Ser Leu Val Leu Val Leu Phe Ser Ala Leu Val Phe	
20 25 30	
tca aat gct ggt tat gct agc tgt gaa gct gtc aca cag aca gac tca	144
Ser Asn Ala Gly Tyr Ala Ser Cys Glu Ala Val Thr Gln Thr Asp Ser	
35 40 45	
cga cct ctg gtt agc cag ggt gtt gca gga ttt tca ggt tcc cag tgg	192
Arg Pro Leu Val Ser Gln Gly Val Ala Gly Phe Ser Gly Ser Gln Trp	
50 55 60	
gat gtg ggt gca gag gca gac ttc tcc tcc tct cac acc ttg gga act	240
Asp Val Gly Ala Glu Ala Asp Phe Ser Ser Ser His Thr Leu Gly Thr	
65 70 75 80	
cac gta gag ttt gca gcg gta agc tgc ttc ttt caa agg gtc tgt gaa	288
His Val Glu Phe Ala Ala Val Ser Cys Phe Phe Gln Arg Val Cys Glu	
85 90 95	
ttc ttt cag ttt tcc tgg tat gtt cct gtg gtg gtt ctt gga gca aaa	336
Phe Phe Gln Phe Ser Trp Tyr Val Pro Val Val Val Leu Gly Ala Lys	
100 105 110	
ctt cac aat cta gaa gag aaa ggc gag gaa tgg cac tgc ctt ctg aaa	384
Leu His Asn Leu Glu Glu Lys Gly Glu Glu Trp His Cys Leu Leu Lys	
115 120 125	
gat gac tgg ctt cta ctt cct tct ctt gtc cag ttc atg aac tcc ctg	432
Asp Asp Trp Leu Leu Leu Pro Ser Leu Val Gln Phe Met Asn Ser Leu	
130 135 140	
gag ttt tgc aat gca gtc ata cag gtg gct cac ccc ttg att cga aat	480
Glu Phe Cys Asn Ala Val Ile Gln Val Ala His Pro Leu Ile Arg Asn	
145 150 155 160	
cag ctt gtc aat tac att tac aat gga ttt ttg gta cca gtc ttg gct	528
Gln Leu Val Asn Tyr Ile Tyr Asn Gly Phe Leu Val Pro Val Leu Ala	
165 170 175	
cct gct ctc cat aag tgg caa ctt gga act gtc aag atg ttc tcc aag	576
Pro Ala Leu His Lys Trp Gln Leu Gly Thr Val Lys Met Phe Ser Lys	

180	185	190	
gct gag tct gtc ata gag aat gca agg tct gct gtg ggc atg gag agg			624
Ala Glu Ser Val Ile Glu Asn Ala Arg Ser Ala Val Gly Met Glu Arg			
195	200	205	
agc agt ggt agc aca agt gcc ata gat ttg cca tct act taa			666
Ser Ser Gly Ser Thr Ser Ala Ile Asp Leu Pro Ser Thr *			
210	215	220	

<210> 146
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 146

Met	Asp	Thr	Ser	Thr	Cys	Ser	Gly	Gly	Ser	Gly	Arg	Gly	Val	Lys	Trp
1				5					10					15	
Thr	Leu	Arg	Glu	Ser	Leu	Val	Leu	Val	Leu	Phe	Ser	Ala	Leu	Val	Phe
			20					25						30	
Ser	Asn	Ala	Gly	Tyr	Ala	Ser	Cys	Glu	Ala	Val	Thr	Gln	Thr	Asp	Ser
		35					40						45		
Arg	Pro	Leu	Val	Ser	Gln	Gly	Val	Ala	Gly	Phe	Ser	Gly	Ser	Gln	Trp
	50					55					60				
Asp	Val	Gly	Ala	Glu	Ala	Asp	Phe	Ser	Ser	Ser	His	Thr	Leu	Gly	Thr
65					70					75					80
His	Val	Glu	Phe	Ala	Ala	Val	Ser	Cys	Phe	Phe	Gln	Arg	Val	Cys	Glu
				85					90					95	
Phe	Phe	Gln	Phe	Ser	Trp	Tyr	Val	Pro	Val	Val	Val	Leu	Gly	Ala	Lys
			100					105					110		
Leu	His	Asn	Leu	Glu	Glu	Lys	Gly	Glu	Glu	Trp	His	Cys	Leu	Leu	Lys
		115					120					125			
Asp	Asp	Trp	Leu	Leu	Leu	Pro	Ser	Leu	Val	Gln	Phe	Met	Asn	Ser	Leu
	130					135					140				
Glu	Phe	Cys	Asn	Ala	Val	Ile	Gln	Val	Ala	His	Pro	Leu	Ile	Arg	Asn
145					150					155					160
Gln	Leu	Val	Asn	Tyr	Ile	Tyr	Asn	Gly	Phe	Leu	Val	Pro	Val	Leu	Ala
			165					170						175	
Pro	Ala	Leu	His	Lys	Trp	Gln	Leu	Gly	Thr	Val	Lys	Met	Phe	Ser	Lys
		180					185					190			
Ala	Glu	Ser	Val	Ile	Glu	Asn	Ala	Arg	Ser	Ala	Val	Gly	Met	Glu	Arg
		195					200					205			

Ser Ser Gly Ser Thr Ser Ala Ile Asp Leu Pro Ser Thr
 210 215 220

<210> 147
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(438)

<400> 147

atg gct cgg gca ggg ggc atg ggg ctg ctg cga tta cag ctg ctt ctg 48
 Met Ala Arg Ala Gly Gly Met Gly Leu Leu Arg Leu Gln Leu Leu Leu
 1 5 10 15

gta ctg ccc aca cta gct tct gcc tgt gtg ccc tgc atc tac ctg gtt 96
 Val Leu Pro Thr Leu Ala Ser Ala Cys Val Pro Cys Ile Tyr Leu Val
 20 25 30

ccc acg tgg acg tcc cta tct gag aca cct ttt gga cca act ctg gac 144
 Pro Thr Trp Thr Ser Leu Ser Glu Thr Pro Phe Gly Pro Thr Leu Asp
 35 40 45

aga ccc tct cca aaa tca aag gtg cgc tgg gct gct aac ctg atc caa 192
 Arg Pro Ser Pro Lys Ser Lys Val Arg Trp Ala Ala Asn Leu Ile Gln
 50 55 60

gac gag atc aat cta gaa gga cct gct ggt gct gca acc cac gct tgg 240
 Asp Glu Ile Asn Leu Glu Gly Pro Ala Gly Ala Ala Thr His Ala Trp
 65 70 75 80

gtc acc ttt gcc aga acc ggg gtc att tgc ttt ggg ggt cct cag gcc 288
 Val Thr Phe Ala Arg Thr Gly Val Ile Cys Phe Gly Gly Pro Gln Ala
 85 90 95

agt gct cag aag gct gct tgt tgt aga tgg agg aca gct cct cag gct 336
 Ser Ala Gln Lys Ala Ala Cys Cys Arg Trp Arg Thr Ala Pro Gln Ala
 100 105 110

ggg aaa tct ctc aat ggg aac tgt gct cag aac aga aca gaa ctt ccc 384
 Gly Lys Ser Leu Asn Gly Asn Cys Ala Gln Asn Arg Thr Glu Leu Pro

115 120 125

gga tac tta gat att tgg gtg gta ttg atc tcc gca tca gtg tcc tcg 432
 Gly Tyr Leu Asp Ile Trp Val Val Leu Ile Ser Ala Ser Val Ser Ser
 130 135 140

ggt tga 438
 Gly *
 145

<210> 148
 <211> 145
 <212> PRT
 <213> Homo sapiens

<400> 148

Met Ala Arg Ala Gly Gly Met Gly Leu Leu Arg Leu Gln Leu Leu Leu
 1 5 10 15
 Val Leu Pro Thr Leu Ala Ser Ala Cys Val Pro Cys Ile Tyr Leu Val
 20 25 30
 Pro Thr Trp Thr Ser Leu Ser Glu Thr Pro Phe Gly Pro Thr Leu Asp
 35 40 45
 Arg Pro Ser Pro Lys Ser Lys Val Arg Trp Ala Ala Asn Leu Ile Gln
 50 55 60
 Asp Glu Ile Asn Leu Glu Gly Pro Ala Gly Ala Ala Thr His Ala Trp
 65 70 75 80
 Val Thr Phe Ala Arg Thr Gly Val Ile Cys Phe Gly Gly Pro Gln Ala
 85 90 95
 Ser Ala Gln Lys Ala Ala Cys Cys Arg Trp Arg Thr Ala Pro Gln Ala
 100 105 110
 Gly Lys Ser Leu Asn Gly Asn Cys Ala Gln Asn Arg Thr Glu Leu Pro
 115 120 125
 Gly Tyr Leu Asp Ile Trp Val Val Leu Ile Ser Ala Ser Val Ser Ser
 130 135 140
 Gly
 145

<210> 149
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(411)

<400> 149

atg	tgg	gtg	ctg	ctg	ctg	ctg	ctg	ttg	gag	gca	ggc	ctc	ggg	gct	ctg	48
Met	Trp	Val	Leu	Leu	Leu	Leu	Leu	Leu	Glu	Ala	Gly	Leu	Gly	Ala	Leu	
1			5						10					15		

act	ctg	gag	ggt	tgt	gaa	ttc	cag	cgg	cac	ggg	gct	gtt	gtg	tgc	ctt	96
Thr	Leu	Glu	Gly	Cys	Glu	Phe	Gln	Arg	His	Gly	Ala	Val	Val	Cys	Leu	
		20					25						30			

gtt	cac	ggc	cat	ctc	cct	tcc	acc	cag	tgt	cta	gcc	cag	tgt	ctg	tac	144
Val	His	Gly	His	Leu	Pro	Ser	Thr	Gln	Cys	Leu	Ala	Gln	Cys	Leu	Tyr	
		35					40					45				

aca	gca	gat	gcg	aag	cta	cgt	gac	gtt	gtc	cgt	gaa	cca	gcc	ggg	ccc	192
Thr	Ala	Asp	Ala	Lys	Leu	Arg	Asp	Val	Val	Arg	Glu	Pro	Ala	Gly	Pro	
	50					55				60						

gcg	ttg	ccc	tac	tca	act	atg	tcg	agg	agc	ccc	ggt	cac	cag	cgg	tct	240
Ala	Leu	Pro	Tyr	Ser	Thr	Met	Ser	Arg	Ser	Pro	Gly	His	Gln	Arg	Ser	
65					70					75					80	

gac	cca	ttt	aac	aat	tct	ggc	tct	acc	gat	atc	cag	ttg	ctc	gcc	cgg	288
Asp	Pro	Phe	Asn	Asn	Ser	Gly	Ser	Thr	Asp	Ile	Gln	Leu	Leu	Ala	Arg	
			85					90						95		

gtc	cac	tca	ccg	aaa	atc	tct	ata	tgt	aat	tct	aag	cct	aaa	aag	acg	336
Val	His	Ser	Pro	Lys	Ile	Ser	Ile	Cys	Asn	Ser	Lys	Pro	Lys	Lys	Thr	
			100					105					110			

ggc	acg	caa	tac	cac	gac	ggc	gac	ctg	ctc	acg	ttc	gtc	ccc	agc	gat	384
Gly	Thr	Gln	Tyr	His	Asp	Gly	Asp	Leu	Leu	Thr	Phe	Val	Pro	Ser	Asp	
	115					120						125				

gca	ctg	ggg	gag	gca	cgt	cgg	cgg	tga								411
Ala	Leu	Gly	Glu	Ala	Arg	Arg	Arg	*								
	130					135										

<210> 150

<400> 150

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<210> 151
<211> 852
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(852)

<400> 151

ctg ggg tct gtg cct gct acc gac gcc cgc tct gtg ccc ctg aag gcc
Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu Lys Ala 96

20 25 30

acg ttc ctg gag gat gtg gcg ggt agt ggg gag gcc gag ggc tcg tcg 144

Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser		
		35					40					45					
gcc	tcc	tcc	ccg	agc	ctc	ccg	cca	ccc	tgg	acc	ccg	gcc	ctc	agc	ccc	192	
Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	Ala	Leu	Ser	Pro		
	50					55					60						
aca	tcg	atg	ggg	ccc	cag	ccc	ata	acc	ctg	ggg	ggc	cca	tca	ccc	ccc	240	
Thr	Ser	Met	Gly	Pro	Gln	Pro	Ile	Thr	Leu	Gly	Gly	Pro	Ser	Pro	Pro		
65					70					75					80		
acc	aac	ttc	ctg	gat	ggg	ata	gtg	gac	ttc	ttc	cgc	cag	tac	gtg	atg	288	
Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr	Val	Met		
				85				90						95			
ctg	att	gct	gtg	gtg	ggc	tcc	ctg	gcc	ttt	ctg	ctg	atg	ttc	atc	gtc	336	
Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	Phe	Leu	Leu	Met	Phe	Ile	Val		
			100				105						110				
tgt	gcc	gcg	gtc	atc	acc	cgg	cag	aag	cag	aag	gcc	tcg	gcc	tat	tac	384	
Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr		
	115					120					125						
cca	tcg	tcc	ttc	ccc	aag	aag	aag	tac	gtg	gac	cag	agt	gac	cgg	gcc	432	
Pro	Ser	Ser	Phe	Pro	Lys	Lys	Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala		
	130					135					140						
ggg	ggc	ccc	cgg	gcc	ttc	agt	gag	gtc	ccc	gac	aga	gcc	ccc	gac	agc	480	
Gly	Gly	Pro	Arg	Ala	Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser		
145					150					155					160		
agg	ccc	gag	gaa	gcc	ctg	gat	tcc	tcc	cgg	cag	ctc	cag	gcc	gac	atc	528	
Arg	Pro	Glu	Glu	Ala	Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile		
				165					170					175			
ttg	gcc	gcc	acc	cag	aac	ctc	aag	tcc	ccc	acc	agg	gct	gca	ctg	ggc	576	
Leu	Ala	Ala	Thr	Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly		
			180				185						190				
ggt	ggg	gac	gga	gcc	agg	atg	gtg	gag	ggc	agg	ggc	gca	gag	gaa	gag	624	
Gly	Gly	Asp	Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu		
		195					200					205					

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	Leu	Leu
1				5				10						15		
Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	Lys	Ala	
			20					25					30			
Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser	
		35					40					45				
Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	Ala	Leu	Ser	Pro	
	50					55					60					
Thr	Ser	Met	Gly	Pro	Gln	Pro	Ile	Thr	Leu	Gly	Gly	Pro	Ser	Pro	Pro	
65					70					75					80	
Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr	Val	Met	
				85				90						95		
Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	Phe	Leu	Leu	Met	Phe	Ile	Val	
			100					105					110			
Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	
		115					120					125				

Pro Ser Ser Phe Pro Lys Lys Lys Tyr Val Asp Gln Ser Asp Arg Ala
 130 135 140
 Gly Gly Pro Arg Ala Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser
 145 150 155 160
 Arg Pro Glu Glu Ala Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile
 165 170 175
 Leu Ala Ala Thr Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly
 180 185 190
 Gly Gly Asp Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu
 195 200 205
 Glu Lys Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val
 210 215 220
 Pro Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 225 230 235 240
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly Ser
 245 250 255
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270
 Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
 275 280

<210> 153
 <211> 696
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(696)

<400> 153

atg ggc gag ggc tcc aaa ggg ccc tgc atg tgc tgt tcc cct gcc tgg	48
Met Gly Glu Gly Ser Lys Gly Pro Cys Met Cys Cys Ser Pro Ala Trp	
1 5 10 15	
atg ccc acc ccc aag ggt cac ctc ctc cag gaa gcc ttc ctt ctt ctc	96
Met Pro Thr Pro Lys Gly His Leu Leu Gln Glu Ala Phe Leu Leu Leu	
20 25 30	
agg ctg agt tgg ctg gtt act gct gtg cct gct ctt gac tgg gga ttc	144
Arg Leu Ser Trp Leu Val Thr Ala Val Pro Ala Leu Asp Trp Gly Phe	
35 40 45	

Val Leu Tyr Thr Leu Ser Gln Ala Leu Pro Asp Ile His Gln Leu Pro
 20 25 30
 Glu Arg Ser Pro Leu Cys Pro Ser Arg Arg Phe Ser Thr Val Ser Thr
 35 40 45
 Ala Ala Ile Ala Gln Arg Thr Gln Gln Gln Gly Ala Ile Leu Glu Ala
 50 55 60
 Glu Ser Ser Pro Tyr Gln Thr Pro Asn Leu Leu Ala Pro Arg Ser Trp
 65 70 75 80
 Ile Ser Trp Cys Leu Glu Leu
 85

<210> 157
 <211> 258
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(258)

<400> 157

atg ctg act gcc atg ctt tcc ctc ctt ggc ttt ctc cag gca ctc ttc 48
 Met Leu Thr Ala Met Leu Ser Leu Leu Gly Phe Leu Gln Ala Leu Phe
 1 5 10 15

aca cac aga tgt gtc tac agt ggc agg ttt ggg agc ctg aag agc ggc 96
 Thr His Arg Cys Val Tyr Ser Gly Arg Phe Gly Ser Leu Lys Ser Gly
 20 25 30

tgt gcc cgg tac tgc aat gcc act gtg aag aac gtt ggc tcc aca agc 144
 Cys Ala Arg Tyr Cys Asn Ala Thr Val Lys Asn Val Gly Ser Thr Ser
 35 40 45

atg agc ctt cct ctg tct gtt cgc aca gtg tta gag cca gtc cag act 192
 Met Ser Leu Pro Leu Ser Val Arg Thr Val Leu Glu Pro Val Gln Thr
 50 55 60

cct tgg cta cct cca gac gta tgc agt agt tca tca tgc ctg caa gcg 240
 Pro Trp Leu Pro Pro Asp Val Cys Ser Ser Ser Ser Cys Leu Gln Ala
 65 70 75 80

gta acg aaa acg att tga 258
 Val Thr Lys Thr Ile *

<210> 158
<211> 85
<212> PRT
<213> Homo sapiens

[illegible]

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<210> 159
<211> 624
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(624)

<400> 159																
atg	gtc	cgc	tgc	ctg	ggg	cct	gcg	ctg	ctg	ctg	ctg	ctg	tta	ctg	ggg	48
Met	Val	Arg	Cys	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gly	
1			5			10			15							
tcg	gcg	agc	tcg	gtc	gga	ggg	aac	cga	tgt	gtg	gac	gcg	gcc	gaa	gcc	96
Ser	Ala	Ser	Ser	Val	Gly	Gly	Asn	Arg	Cys	Val	Asp	Ala	Ala	Glu	Ala	
20			25			30										
tgc	acg	gcg	gac	gcg	cgg	tgc	cag	cgt	ttg	cgc	tcc	gag	tat	gtg	gcg	144
Cys	Thr	Ala	Asp	Ala	Arg	Cys	Gln	Arg	Leu	Arg	Ser	Glu	Tyr	Val	Ala	
35			40			45										

cag tgc ctg ggc cgg gct gcg cag ggg ggc tgt ccc gcg ccc gct gcc	192
Gln Cys Leu Gly Arg Ala Ala Gln Gly Gly Cys Pro Ala Pro Ala Ala	
50 55 60	
gcc ggg ccc tgc gcc gct tct tcg ccc gcg ggc gcc cgc gct cac cca	240
Ala Gly Pro Cys Ala Ala Ser Ser Pro Ala Gly Ala Arg Ala His Pro	
65 70 75 80	
cgc act gct ctt ctg ccc gtg cgc cgc ccg gct gcg ccg agc gtc gga	288
Arg Thr Ala Leu Leu Pro Val Arg Arg Pro Ala Ala Pro Ser Val Gly	
85 90 95	
gca ccc ttc gtg ccc tcc tgc gcc ttt tcg ggg ccc ggc cgc ccg ccc	336
Ala Pro Phe Val Pro Ser Cys Ala Phe Ser Gly Pro Gly Arg Pro Pro	
100 105 110	
tcc tgc ctt gag ccc tta aac ttc tgc gag cga cgg aac tgc agg atc	384
Ser Cys Leu Glu Pro Leu Asn Phe Cys Glu Arg Arg Asn Cys Arg Ile	
115 120 125	
ccc ggc ggc gcg gcc gct ggc gag gcg ccc agc gcc ccc gac ggc tgc	432
Pro Gly Gly Ala Ala Ala Gly Glu Ala Pro Ser Ala Pro Asp Gly Cys	
130 135 140	
ctg ctg gac cag agg cgc ccg ctg cct gcg ccc tac gcg ggc ctc gtg	480
Leu Leu Asp Gln Arg Arg Pro Leu Pro Ala Pro Tyr Ala Gly Leu Val	
145 150 155 160	
ggt acg cgc ggc cgg gat ccg ggc gag ggc ggg ggt tct cca ggg gat	528
Gly Thr Arg Gly Arg Asp Pro Gly Glu Gly Gly Gly Ser Pro Gly Asp	
165 170 175	
atc tcc gcc ggc acc gcc gtc acc cct aac tac gtg gac aac gtg agc	576
Ile Ser Ala Gly Thr Ala Val Thr Pro Asn Tyr Val Asp Asn Val Ser	
180 185 190	
gcg cgt ggc gcc ctg gtg cga ctg cgg agc cag cgg gaa ccg gcg tga	624
Ala Arg Gly Ala Leu Val Arg Leu Arg Ser Gln Arg Glu Pro Ala *	
195 200 205	

160

<211> 207
 <212> PRT
 <213> Homo sapiens

<400> 160

Met	Val	Arg	Cys	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly
1				5				10					15	
Ser	Ala	Ser	Ser	Val	Gly	Gly	Asn	Arg	Cys	Val	Asp	Ala	Ala	Glu
			20				25					30		
Cys	Thr	Ala	Asp	Ala	Arg	Cys	Gln	Arg	Leu	Arg	Ser	Glu	Tyr	Val
		35					40					45		
Gln	Cys	Leu	Gly	Arg	Ala	Ala	Gln	Gly	Gly	Cys	Pro	Ala	Pro	Ala
	50					55				60				
Ala	Gly	Pro	Cys	Ala	Ala	Ser	Ser	Pro	Ala	Gly	Ala	Arg	Ala	His
65					70					75				80
Arg	Thr	Ala	Leu	Leu	Pro	Val	Arg	Arg	Pro	Ala	Ala	Pro	Ser	Val
			85						90				95	
Ala	Pro	Phe	Val	Pro	Ser	Cys	Ala	Phe	Ser	Gly	Pro	Gly	Arg	Pro
		100					105					110		
Ser	Cys	Leu	Glu	Pro	Leu	Asn	Phe	Cys	Glu	Arg	Arg	Asn	Cys	Arg
	115					120						125		
Pro	Gly	Gly	Ala	Ala	Ala	Gly	Glu	Ala	Pro	Ser	Ala	Pro	Asp	Gly
	130					135					140			
Leu	Leu	Asp	Gln	Arg	Arg	Pro	Leu	Pro	Ala	Pro	Tyr	Ala	Gly	Leu
145					150					155				160
Gly	Thr	Arg	Gly	Arg	Asp	Pro	Gly	Glu	Gly	Gly	Gly	Ser	Pro	Gly
			165					170					175	
Ile	Ser	Ala	Gly	Thr	Ala	Val	Thr	Pro	Asn	Tyr	Val	Asp	Asn	Val
		180					185					190		
Ala	Arg	Gly	Ala	Leu	Val	Arg	Leu	Arg	Ser	Gln	Arg	Glu	Pro	Ala
		195					200					205		

<210> 161
 <211> 423
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(423)

<400> 161

atg tcc acc acc aca tgc caa gtg gtg gcg ttc ctc ctg tcc atc ctg

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile	Leu	
1				5					10					15		
ggg	ctg	gcc	ggc	tgc	atc	gcg	gcc	acc	ggg	atg	gac	atg	tgg	agc	acc	96
Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp	Ser	Thr	
			20					25					30			
cag	gac	ctg	tac	gac	aac	ccc	gtc	acc	tcc	gtg	ttc	cag	tac	gaa	ggg	144
Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln	Tyr	Glu	Gly	
			35				40					45				
ctc	tgg	agg	agc	tgc	gtg	agg	cag	agt	tca	ggc	ttc	acc	gaa	tgc	agg	192
Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe	Thr	Glu	Cys	Arg	
	50					55					60					
ccc	tat	ttc	acc	atc	ctg	gga	ctt	cca	gtc	tct	tac	tcc	ccc	atc	ctg	240
Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Val	Ser	Tyr	Ser	Pro	Ile	Leu	
	65				70				75					80		
ttt	ctt	ctg	tcc	ttt	cag	tat	acc	ttg	gac	ttg	gtc	ctg	gac	atc	cat	288
Phe	Leu	Leu	Ser	Phe	Gln	Tyr	Thr	Leu	Asp	Leu	Val	Leu	Asp	Ile	His	
				85				90						95		
tgc	tcc	tgc	tcc	cct	gaa	ttc	ccc	cct	cca	cca	ccc	caa	ctg	tcc	tct	336
Cys	Ser	Cys	Ser	Pro	Glu	Phe	Pro	Pro	Pro	Pro	Pro	Gln	Leu	Ser	Ser	
			100				105					110				
cac	aaa	tct	tcc	tcc	aaa	cct	cct	caa	gcc	ccc	aaa	ttg	aat	aaa	gat	384
His	Lys	Ser	Ser	Ser	Lys	Pro	Pro	Gln	Ala	Pro	Lys	Leu	Asn	Lys	Asp	
			115				120					125				
tcc	aca	agt	ctc	tgt	acc	aaa	ccc	aga	gca	ttc	tca	tag				423
Ser	Thr	Ser	Leu	Cys	Thr	Lys	Pro	Arg	Ala	Phe	Ser	*				
	130					135					140					

<210> 162

<211> 140

<212> PRT

<213> Homo sapiens

<400> 162

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu

1 5 10 15
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20 25 30
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35 40 45
 Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50 55 60
 Pro Tyr Phe Thr Ile Leu Gly Leu Pro Val Ser Tyr Ser Pro Ile Leu
 65 70 75 80
 Phe Leu Leu Ser Phe Gln Tyr Thr Leu Asp Leu Val Leu Asp Ile His
 85 90 95
 Cys Ser Cys Ser Pro Glu Phe Pro Pro Pro Pro Gln Leu Ser Ser
 100 105 110
 His Lys Ser Ser Ser Lys Pro Pro Gln Ala Pro Lys Leu Asn Lys Asp
 115 120 125
 Ser Thr Ser Leu Cys Thr Lys Pro Arg Ala Phe Ser
 130 135 140

<210> 163

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(612)

<400> 163

atg gtc cgg ctc tgc cag gcc ctg ctg ctg tta gtg gcc act gtg gcc 48
 Met Val Arg Leu Cys Gln Ala Leu Leu Leu Leu Val Ala Thr Val Ala
 1 5 10 15

ctt gca tcc aga aga ttc caa gcc tgg ggc tca aca aag gtg gtg agg 96
 Leu Ala Ser Arg Arg Phe Gln Ala Trp Gly Ser Thr Lys Val Val Arg
 20 25 30

aca ttc caa gat atc cct caa aac tac gtc tat gtg cag cag gca ctc 144
 Thr Phe Gln Asp Ile Pro Gln Asn Tyr Val Tyr Val Gln Gln Ala Leu
 35 40 45

tgg ttc gcc atg aag gag tat aac aag gcc agc ttt agt ata aca agt 192
 Trp Phe Ala Met Lys Glu Tyr Asn Lys Ala Ser Phe Ser Ile Thr Ser
 50 55 60

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<210> 164
<211> 203
<212> PRT
<213> Homo sapiens
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<400> 164

Met Val Arg Leu Cys Gln Ala Leu Leu Leu Leu Val Ala Thr Val Ala
 1 5 10 15
 Leu Ala Ser Arg Arg Phe Gln Ala Trp Gly Ser Thr Lys Val Val Arg
 20 25 30
 Thr Phe Gln Asp Ile Pro Gln Asn Tyr Val Tyr Val Gln Gln Ala Leu
 35 40 45
 Trp Phe Ala Met Lys Glu Tyr Asn Lys Ala Ser Phe Ser Ile Thr Ser
 50 55 60
 Ser Ala Leu Gly Leu Ser Ala Ala Ala Glu Phe Val Gln Cys Glu Cys
 65 70 75 80
 Trp Arg Lys Glu His Leu Ile Pro Ser Gly Leu Glu Pro His Gly Asn
 85 90 95
 Glu Arg Ile Pro Val Tyr Leu Ala Pro Gly Leu Val Ala Phe His Arg
 100 105 110
 Cys Thr Gln Val Thr Asp Ser Leu Glu Tyr Tyr Ile Glu Val Lys Ile
 115 120 125
 Ala Arg Thr Ile Cys Lys Lys Ile Ser Glu Asp Glu Asn Cys Ala Phe
 130 135 140
 Gln Glu Asp Pro Lys Met Gln Lys Ser Gln Arg Ser Arg Leu Leu Leu
 145 150 155 160
 Leu Gln Ala Lys Met Gly Asp Ser Pro Ser Gln Ala Arg Leu Phe Ser
 165 170 175
 Asp Gly Asp Cys His Lys Gly Lys Phe Ile Thr Glu Glu Thr Gly Leu
 180 185 190
 Ile Lys Lys Ser Leu Thr Leu Leu Val Val Asp
 195 200

<210> 165

<211> 534

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(534)

<400> 165

atg ggt att cag aac tca cca gca ctc ctc ctg atg gct gtc att gtg 48
 Met Gly Ile Gln Asn Ser Pro Ala Leu Leu Leu Met Ala Val Ile Val
 1 5 10 15

ttt ggc aca ttt gct gta agt gta gac agt gac ttg tac act gaa ctg 96

Phe	Gly	Thr	Phe	Ala	Val	Ser	Val	Asp	Ser	Asp	Leu	Tyr	Thr	Glu	Leu			
			20				25						30					
cgc	tgc	gtg	tat	gtg	aag	tca	acc	ttt	gta	ctt	cat	ccc	aga	aac	atc	144		
Arg	Cys	Val	Tyr	Val	Lys	Ser	Thr	Phe	Val	Leu	His	Pro	Arg	Asn	Ile			
			35				40						45					
cac	aat	ttg	gag	ttg	gtc	tca	gca	gga	ccc	cat	tgc	agc	aaa	gac	gaa	192		
His	Asn	Leu	Glu	Leu	Val	Ser	Ala	Gly	Pro	His	Cys	Ser	Lys	Asp	Glu			
			50				55						60					
gta	atg	atg	gag	cag	tgc	cta	agt	tta	ggc	tcc	tcc	aaa	atg	cag	aat	240		
Val	Met	Met	Glu	Gln	Cys	Leu	Ser	Leu	Gly	Ser	Ser	Lys	Met	Gln	Asn			
			65				70						80					
ttg	agt	cat	gag	cct	gcc	atg	cag	agg	gag	gaa	gga	cgt	tat	gca	gga	288		
Leu	Ser	His	Glu	Pro	Ala	Met	Gln	Arg	Glu	Glu	Gly	Arg	Tyr	Ala	Gly			
			85						90						95			
tac	aaa	aga	aga	ggt	cat	gtt	ata	cag	ccc	tgg	ctt	cca	cgg	aca	cta	336		
Tyr	Lys	Arg	Arg	Gly	His	Val	Ile	Gln	Pro	Trp	Leu	Pro	Arg	Thr	Leu			
			100						105						110			
aca	ctg	aat	tca	aat	ttt	gac	act	gat	aat	ctg	ttg	cca	cca	aat	gga	384		
Thr	Leu	Asn	Ser	Asn	Phe	Asp	Thr	Asp	Asn	Leu	Leu	Pro	Pro	Asn	Gly			
			115						120						125			
aaa	cgt	aaa	caa	ggt	att	cta	agt	gtg	att	aga	gaa	tat	gca	aaa	caa	432		
Lys	Arg	Lys	Gln	Gly	Ile	Leu	Ser	Val	Ile	Arg	Glu	Tyr	Ala	Lys	Gln			
			130						135						140			
gga	aca	agt	aga	aca	ttc	ttc	tct	gga	atc	cga	gac	gat	ggc	tgt	act	480		
Gly	Thr	Ser	Arg	Thr	Phe	Phe	Ser	Gly	Ile	Arg	Asp	Asp	Gly	Cys	Thr			
			145						150						155			
ttc	aca	gag	agc	atg	atg	tta	gat	gta	cat	gaa	ata	acg	cta	aac	cga	528		
Phe	Thr	Glu	Ser	Met	Met	Leu	Asp	Val	His	Glu	Ile	Thr	Leu	Asn	Arg			
			165						170						175			
aaa	tga															534		
Lys	*																	

48

Met	Leu	Ser	Lys	Thr	Glu	Gln	Val	Gln	Leu	Gly	Met	Ala	Leu	Ala	Leu	
1				5					10					15		
gct	gcc	ttg	agc	aga	ggc	aga	tct	gtc	ctg	gcc	ttc	ctc	ctg	atc	tct	96
Ala	Ala	Leu	Ser	Arg	Gly	Arg	Ser	Val	Leu	Ala	Phe	Leu	Leu	Ile	Ser	
			20					25					30			
ggt	gaa	gat	gca	gaa	ggc	aaa	tgc	tta	gca	ttt	tat	ctg	ttc	tgc	atc	144
Gly	Glu	Asp	Ala	Glu	Gly	Lys	Cys	Leu	Ala	Phe	Tyr	Leu	Phe	Cys	Ile	
		35					40					45				
cca	ccg	gcg	ggc	ata	att	ccc	agc	tta	gtc	ttt	gac	aag	tct	tcc	aag	192
Pro	Pro	Ala	Gly	Ile	Ile	Pro	Ser	Leu	Val	Phe	Asp	Lys	Ser	Ser	Lys	
	50					55					60					
cct	cag	gcc	cca	gag	ccc	atg	acg	cca	gca	cgc	tcc	ttt	tgg	acg	gtt	240
Pro	Gln	Ala	Pro	Glu	Pro	Met	Thr	Pro	Ala	Arg	Ser	Phe	Trp	Thr	Val	
65					70				75						80	
gtt	tat	gtc	gtc	gtt	atc	tat	cag	aac	agc	acc	tat	tac	gat	gga	ggc	288
Val	Tyr	Val	Val	Val	Ile	Tyr	Gln	Asn	Ser	Thr	Tyr	Tyr	Asp	Gly	Gly	
				85					90					95		
ggc	tgc	cat	aac	agc	ctt	aag	gtg	acc	agc	agc	ccc	gcc	att	gcc	atc	336
Gly	Cys	His	Asn	Ser	Leu	Lys	Val	Thr	Ser	Ser	Pro	Ala	Ile	Ala	Ile	
			100					105					110			
gcc	acc	gcc	gcc	gcc	gct	gcc	atg	gtc	tcc	gtg	gac	cct	gag	aac	ctc	384
Ala	Thr	Ala	Ala	Ala	Ala	Ala	Met	Val	Ser	Val	Asp	Pro	Glu	Asn	Leu	
		115					120					125				
cgg	ggc	ccg	tcc	ccc	tcc	agc	gtg	cag	ccg	cgc	cac	ttc	ctg	acc	ttg	432
Arg	Gly	Pro	Ser	Pro	Ser	Ser	Val	Gln	Pro	Arg	His	Phe	Leu	Thr	Leu	
	130					135					140					
gca	ccc	atc	aaa	ata	ccc	ctc	cgg	acg	tcc	ccc	gtc	tca	ggc	atg	cgt	480
Ala	Pro	Ile	Lys	Ile	Pro	Leu	Arg	Thr	Ser	Pro	Val	Ser	Gly	Met	Arg	
145					150					155					160	
gtc	cat	cca	cta	act	gta	acc	tgc	acg	ctt	cgt	gac	cca	gac	atc	ctt	528
Val	His	Pro	Leu	Thr	Val	Thr	Cys	Thr	Leu	Arg	Asp	Pro	Asp	Ile	Leu	
				165					170					175		

gtg aaa tgc gtg ttt ctt caa act tag
 Val Lys Cys Val Phe Leu Gln Thr *
 180

555

<210> 168
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 168
 Met Leu Ser Lys Thr Glu Gln Val Gln Leu Gly Met Ala Leu Ala Leu
 1 5 10 15
 Ala Ala Leu Ser Arg Gly Arg Ser Val Leu Ala Phe Leu Leu Ile Ser
 20 25 30
 Gly Glu Asp Ala Glu Gly Lys Cys Leu Ala Phe Tyr Leu Phe Cys Ile
 35 40 45
 Pro Pro Ala Gly Ile Ile Pro Ser Leu Val Phe Asp Lys Ser Ser Lys
 50 55 60
 Pro Gln Ala Pro Glu Pro Met Thr Pro Ala Arg Ser Phe Trp Thr Val
 65 70 75 80
 Val Tyr Val Val Val Ile Tyr Gln Asn Ser Thr Tyr Tyr Asp Gly Gly
 85 90 95
 Gly Cys His Asn Ser Leu Lys Val Thr Ser Ser Pro Ala Ile Ala Ile
 100 105 110
 Ala Thr Ala Ala Ala Ala Ala Met Val Ser Val Asp Pro Glu Asn Leu
 115 120 125
 Arg Gly Pro Ser Pro Ser Ser Val Gln Pro Arg His Phe Leu Thr Leu
 130 135 140
 Ala Pro Ile Lys Ile Pro Leu Arg Thr Ser Pro Val Ser Gly Met Arg
 145 150 155 160
 Val His Pro Leu Thr Val Thr Cys Thr Leu Arg Asp Pro Asp Ile Leu
 165 170 175
 Val Lys Cys Val Phe Leu Gln Thr
 180

<210> 169
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1)...(552)

<400> 169

atg gct ctc cgg gtc agc ctg tgt ctt ctc ctc cgt gca tcc tca ctt	48
Met Ala Leu Arg Val Ser Leu Cys Leu Leu Leu Arg Ala Ser Ser Leu	
1 5 10 15	
agc tgt gct gca cca gga aac ccc atg gct gga aac cgt aag ctc ccc	96
Ser Cys Ala Ala Pro Gly Asn Pro Met Ala Gly Asn Arg Lys Leu Pro	
20 25 30	
aag gaa gaa ggg act act tct tac cac aag ggt gaa gat gag tca ttt	144
Lys Glu Glu Gly Thr Thr Ser Tyr His Lys Gly Glu Asp Glu Ser Phe	
35 40 45	
gtc aat act tca aca gaa aag aaa atg agt aaa gat tgg aag tct gat	192
Val Asn Thr Ser Thr Glu Lys Lys Met Ser Lys Asp Trp Lys Ser Asp	
50 55 60	
gac agc atg cct gtc tgt agc tct gga aag ggc atg ggc atc tca aca	240
Asp Ser Met Pro Val Cys Ser Ser Gly Lys Gly Met Gly Ile Ser Thr	
65 70 75 80	
ggc ata cag gag agc cac aaa gag cat ctc aga gac caa ggc aca cgg	288
Gly Ile Gln Glu Ser His Lys Glu His Leu Arg Asp Gln Gly Thr Arg	
85 90 95	
gac ttt gca tta ctt cca aag gtc atg gtc acc gtc aca att tcc atg	336
Asp Phe Ala Leu Leu Pro Lys Val Met Val Thr Val Thr Ile Ser Met	
100 105 110	
acc tta ctc atg ctg gca act ctg ctt gaa acg tcc tta act cat ctt	384
Thr Leu Leu Met Leu Ala Thr Leu Leu Glu Thr Ser Leu Thr His Leu	
115 120 125	
ctc cac ctg gaa aaa atc caa acc ttt gat gaa gtt tgg cac tat ggc	432
Leu His Leu Glu Lys Ile Gln Thr Phe Asp Glu Val Trp His Tyr Gly	
130 135 140	
cat gac agc ctc cag ata gga gaa ggg tct ggc ttc att gac att tcc	480
His Asp Ser Leu Gln Ile Gly Glu Gly Ser Gly Phe Ile Asp Ile Ser	
145 150 155 160	

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(429)

<400> 171

atg gag acc ttt cct ctg ctg ctg ctc agc ctg ggc ctg gtt ctt gca	48
Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val Leu Ala	
1 5 10 15	
 gaa gca tca gaa agc aca atg aag ata att aaa gaa gaa ttt aca gac	96
Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp	
20 25 30	
 gaa gag atg caa tat gac atg gca aaa agt ggc caa gaa aaa cag acc	144
Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr	
35 40 45	
 att gag ata tta atg aac ccg atc ctg tta gtt aaa aat acc agc ctc	192
Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu	
50 55 60	
 agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc aga agt	240
Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser	
65 70 75 80	
 tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac aaa gag	288
Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu	
85 90 95	
 tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca aac gga	336
Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly	
100 105 110	
 tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa gtg atg	384
Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met	
115 120 125	
 cgc agg gtc cac agg gcc ccc agc tgc aag ttg ggg gtt ctt taa	429
Arg Arg Val His Arg Ala Pro Ser Cys Lys Leu Gly Val Leu *	
130 135 140	

<210> 172
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 172

Met	Glu	Thr	Phe	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Gly	Leu	Val	Leu	Ala
1				5					10					15	
Glu	Ala	Ser	Glu	Ser	Thr	Met	Lys	Ile	Ile	Lys	Glu	Glu	Phe	Thr	Asp
			20					25					30		
Glu	Glu	Met	Gln	Tyr	Asp	Met	Ala	Lys	Ser	Gly	Gln	Glu	Lys	Gln	Thr
		35					40					45			
Ile	Glu	Ile	Leu	Met	Asn	Pro	Ile	Leu	Leu	Val	Lys	Asn	Thr	Ser	Leu
50						55					60				
Ser	Met	Ser	Lys	Asp	Asp	Met	Ser	Ser	Thr	Leu	Leu	Thr	Phe	Arg	Ser
65				70					75					80	
Leu	His	Tyr	Asn	Asp	Pro	Lys	Gly	Asn	Ser	Ser	Gly	Asn	Asp	Lys	Glu
			85					90					95		
Cys	Cys	Asn	Asp	Met	Thr	Val	Trp	Arg	Lys	Val	Ser	Glu	Ala	Asn	Gly
		100					105					110			
Ser	Cys	Lys	Trp	Ser	Asn	Asn	Phe	Ile	Arg	Ser	Ser	Thr	Glu	Val	Met
		115				120						125			
Arg	Arg	Val	His	Arg	Ala	Pro	Ser	Cys	Lys	Leu	Gly	Val	Leu		
130						135					140				

<210> 173
 <211> 534
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(534)

<400> 173

atg	gct	ctc	agc	ctc	tgg	ccc	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	48
Met	Ala	Leu	Ser	Leu	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
1				5				10					15			
ctg	ctg	tcc	ttt	gca	ggg	gga	tcc	tct	aga	gtc	gac	ctg	cag	gca	gcg	96
Leu	Leu	Ser	Phe	Ala	Gly	Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Ala	
			20				25					30				

agc tcg cag cgg aag tgt gag agg aga gtt tct gtg ccc ttc tcc ccc 144
 Ser Ser Gln Arg Lys Cys Glu Arg Arg Val Ser Val Pro Phe Ser Pro
 35 40 45

gcc aaa aag aaa acc caa agg gca aga aga aat ttg ggc caa aaa tgc 192
 Ala Lys Lys Lys Thr Gln Arg Ala Arg Arg Asn Leu Gly Gln Lys Cys
 50 55 60

cca aaa gct cgt cac ctt ttt aaa aaa tgg ggt ccc cgt cac aaa att 240
 Pro Lys Ala Arg His Leu Phe Lys Lys Trp Gly Pro Arg His Lys Ile
 65 70 75 80

gtg tcc acc ccc aac act tcc tgg ggg ggc caa agg tct ttg gaa aaa 288
 Val Ser Thr Pro Asn Thr Ser Trp Gly Gly Gln Arg Ser Leu Glu Lys
 85 90 95

agc ttt gcc aaa tca ctc tta gct ttg gac cca cgc tgg gcc gtc ttt 336
 Ser Phe Ala Lys Ser Leu Leu Ala Leu Asp Pro Arg Trp Ala Val Phe
 100 105 110

ggg gac ttt acg ggg gtc tcc agt ggg tta acc aag gaa gac aaa ggt 384
 Gly Asp Phe Thr Gly Val Ser Ser Gly Leu Thr Lys Glu Asp Lys Gly
 115 120 125

ttc gaa gat cca tct caa ggc cta ttg gtt ata aag agg ttt aag ggt 432
 Phe Glu Asp Pro Ser Gln Gly Leu Leu Val Ile Lys Arg Phe Lys Gly
 130 135 140

ttt aag ttg ggg cct ttc cga ttc cgg agg gaa ccc gtc atc ccg ata 480
 Phe Lys Leu Gly Pro Phe Arg Phe Arg Arg Glu Pro Val Ile Pro Ile
 145 150 155 160

aag cag ttg gga tac ccc agg ggc tct gct aga agc tca ggc cag ggt 528
 Lys Gln Leu Gly Tyr Pro Arg Gly Ser Ala Arg Ser Ser Gly Gln Gly
 165 170 175

ggt tga 534
 Gly *

174

<211> 177
<212> PRT
<213> Homo sapiens

<400> 174

Met Ala Leu Ser Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Leu
1 5 10 15
Leu Leu Ser Phe Ala Gly Gly Ser Ser Arg Val Asp Leu Gln Ala Ala
20 25 30
Ser Ser Gln Arg Lys Cys Glu Arg Arg Val Ser Val Pro Phe Ser Pro
35 40 45
Ala Lys Lys Lys Thr Gln Arg Ala Arg Arg Asn Leu Gly Gln Lys Cys
50 55 60
Pro Lys Ala Arg His Leu Phe Lys Lys Trp Gly Pro Arg His Lys Ile
65 70 75 80
Val Ser Thr Pro Asn Thr Ser Trp Gly Gly Gln Arg Ser Leu Glu Lys
85 90 95
Ser Phe Ala Lys Ser Leu Leu Ala Leu Asp Pro Arg Trp Ala Val Phe
100 105 110
Gly Asp Phe Thr Gly Val Ser Ser Gly Leu Thr Lys Glu Asp Lys Gly
115 120 125
Phe Glu Asp Pro Ser Gln Gly Leu Leu Val Ile Lys Arg Phe Lys Gly
130 135 140
Phe Lys Leu Gly Pro Phe Arg Phe Arg Arg Glu Pro Val Ile Pro Ile
145 150 155 160
Lys Gln Leu Gly Tyr Pro Arg Gly Ser Ala Arg Ser Ser Gly Gln Gly
165 170 175
Gly

<210> 175
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(468)

<400> 175

atg ggt ttg ggc tcg ctg ctt gct ttt tgg ccg gga agc cgg tgc gtc
Met Gly Leu Gly Ser Leu Leu Ala Phe Trp Pro Gly Ser Arg Cys Val
1 5 10 15

48

ccg ttg gtt gtg gtt tgg gcc tac cgc cgg gtg tgg cgg gtg ggt gct	96
Pro Leu Val Val Val Trp Ala Tyr Arg Arg Val Trp Arg Val Gly Ala	
20 25 30	
ggg gtc ccc ggg ggg ggt ggt cta ttt aaa aaa aaa aag ctc ctc	144
Gly Val Pro Gly Gly Gly Gly Leu Phe Lys Lys Lys Lys Lys Leu Leu	
35 40 45	
gtt cgg aag gtt cga tcg gcc tta aag aac gcc tgc atg gtg ggt cta	192
Val Arg Lys Val Arg Ser Ala Leu Lys Asn Ala Cys Met Val Gly Leu	
50 55 60	
caa gtc att aaa tcc cag act gcc agc ggt cac aga agt cag gag aaa	240
Gln Val Ile Lys Ser Gln Thr Ala Ser Gly His Arg Ser Gln Glu Lys	
65 70 75 80	
gac ctg gaa cag att ctt tct cag agt atc aac aag gaa cca atc ctg	288
Asp Leu Glu Gln Ile Leu Ser Gln Ser Ile Asn Lys Glu Pro Ile Leu	
85 90 95	
cat gac tcc ttg ggg tac cga gct cga att cgt aat cat ggc atc ggc	336
His Asp Ser Leu Gly Tyr Arg Ala Arg Ile Arg Asn His Gly Ile Gly	
100 105 110	
gcc cgc gtt gtt ccg ggt ttg gct ggt gtt gtt cgg tct tct cgg tgc	384
Ala Arg Val Val Pro Gly Leu Ala Gly Val Val Arg Ser Ser Arg Cys	
115 120 125	
cgg cgt atg gcg gcc cta gtt tcg cgt cgc ggc acc ggc att ttt gtg	432
Arg Arg Met Ala Ala Leu Val Ser Arg Arg Gly Thr Gly Ile Phe Val	
130 135 140	
ttg tac gaa gcg gag gaa aag aag act gcg tgc tga	468
Leu Tyr Glu Ala Glu Glu Lys Lys Thr Ala Cys *	
145 150 155	

<210> 176

<211> 155

<212> PRT

<213> Homo sapiens

<400> 176

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Met Gly Leu Gly Ser Leu Leu Ala Phe Trp Pro Gly Ser Arg Cys Val
 1           5           10           15
Pro Leu Val Val Val Trp Ala Tyr Arg Arg Val Trp Arg Val Gly Ala
      20           25           30
Gly Val Pro Gly Gly Gly Gly Leu Phe Lys Lys Lys Lys Lys Leu Leu
      35           40           45
Val Arg Lys Val Arg Ser Ala Leu Lys Asn Ala Cys Met Val Gly Leu
      50           55           60
Gln Val Ile Lys Ser Gln Thr Ala Ser Gly His Arg Ser Gln Glu Lys
65           70           75           80
Asp Leu Glu Gln Ile Leu Ser Gln Ser Ile Asn Lys Glu Pro Ile Leu
      85           90           95
His Asp Ser Leu Gly Tyr Arg Ala Arg Ile Arg Asn His Gly Ile Gly
      100          105          110
Ala Arg Val Val Pro Gly Leu Ala Gly Val Val Arg Ser Ser Arg Cys
      115          120          125
Arg Arg Met Ala Ala Leu Val Ser Arg Arg Gly Thr Gly Ile Phe Val
      130          135          140
Leu Tyr Glu Ala Glu Glu Lys Lys Thr Ala Cys
145          150          155

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<210> 177

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(288)

<400> 177

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atg att tta tta cac ctt ctg gat ttg gca aag atc aac gct caa agt      48
Met Ile Leu Leu His Leu Leu Asp Leu Ala Lys Ile Asn Ala Gln Ser
 1           5           10           15

gcg acg gcc tct tcg aat tgg gat cgc ccc aag cct agg aat ctt atc      96
Ala Thr Ala Ser Ser Asn Trp Asp Arg Pro Lys Pro Arg Asn Leu Ile
      20           25           30

cct ccg att tat gcg aac ccg aca atg tac gtg gag cgg gag gtt gct      144
Pro Pro Ile Tyr Ala Asn Pro Thr Met Tyr Val Glu Arg Glu Val Ala
      35           40           45

```


atg gtg tgc ttc ctc aga gtg ctg tgg ctt ctc ctc ttg att ctc tct	48
Met Val Cys Phe Leu Arg Val Leu Trp Leu Leu Leu Leu Ile Leu Ser	
1 5 10 15	
tct ctg cta acc cag aaa acc cgc act gct gag aag aaa tat ggc aca	96
Ser Leu Leu Thr Gln Lys Thr Arg Thr Ala Glu Lys Lys Tyr Gly Thr	
20 25 30	
caa cag ttt ctt cct ctg ctc cat gct gga cca agt ggc ttc ata gct	144
Gln Gln Phe Leu Pro Leu Leu His Ala Gly Pro Ser Gly Phe Ile Ala	
35 40 45	
gcc cag cca gag aca tca aca aca gcc atg ggt gcc aca gct agg agc	192
Ala Gln Pro Glu Thr Ser Thr Thr Ala Met Gly Ala Thr Ala Arg Ser	
50 55 60	
ttc tac ctg gaa cat ccg tta gct ttt gag att cta ttt ttt gcc tta	240
Phe Tyr Leu Glu His Pro Leu Ala Phe Glu Ile Leu Phe Phe Ala Leu	
65 70 75 80	
tat gtg agg gac tgc aat gtg gaa gaa agg agg agg gaa aca ccg gcc	288
Tyr Val Arg Asp Cys Asn Val Glu Glu Arg Arg Arg Glu Thr Pro Ala	
85 90 95	
ctg ggc gcc agg tct cct cct cta gag ctc tcc cca gtt gtg acg ctc	336
Leu Gly Ala Arg Ser Pro Pro Leu Glu Leu Ser Pro Val Val Thr Leu	
100 105 110	
tta ttc aag gcg ttc tcc ccc ccg gac aca gac ttg ctt cat cag cgt	384
Leu Phe Lys Ala Phe Ser Pro Pro Asp Thr Asp Leu Leu His Gln Arg	
115 120 125	
aca gtg cag gct aaa cag tga	405
Thr Val Gln Ala Lys Gln *	
130	

<210> 180

<211> 134

<212> PRT

<213> Homo sapiens

<400> 180

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<210> 181
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(366)
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<400> 181																
atg	gcg	acg	ccc	agg	ggc	ctg	ggg	gcc	ctg	ctc	ctg	ctc	ctc	ctg	ctc	48
Met	Ala	Thr	Pro	Arg	Gly	Leu	Gly	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
1			5			10			15							
ccg	acc	tca	ggg	cca	cag	gca	ccc	agt	ctg	agc	ttg	tct	ggg	ctg	gcg	96
Pro	Thr	Ser	Gly	Pro	Gln	Ala	Pro	Ser	Leu	Ser	Leu	Ser	Gly	Leu	Ala	
			20			25			30							
ggc	agc	ccc	agc	gaa	tca	cat	gag	gat	gcc	tgg	ggc	ggg	ggg	aca	gag	144
Gly	Ser	Pro	Ser	Glu	Ser	His	Glu	Asp	Ala	Trp	Gly	Gly	Gly	Thr	Glu	
35						40						45				
aac	cac	tct	gaa	aca	cac	tgt	gcc	aac	caa	aag	gct	ccc	cgg	act	gtc	192
Asn	His	Ser	Glu	Thr	His	Cys	Ala	Asn	Gln	Lys	Ala	Pro	Arg	Thr	Val	

50	55	60	
cca gca gtt ctg agg agt gcc tgt ccc cgt ttt aca gac aag gag atg			240
Pro Ala Val Leu Arg Ser Ala Cys Pro Arg Phe Thr Asp Lys Glu Met			
65	70	75	80
gag ggt gac cga aaa caa ctc aaa gca atc cac caa gcc tct agt cag			288
Glu Gly Asp Arg Lys Gln Leu Lys Ala Ile His Gln Ala Ser Ser Gln			
	85	90	95
cag ctg ctg tgt gtc aac tac cca gag gaa aca ggt gaa aac caa atg			336
Gln Leu Leu Cys Val Asn Tyr Pro Glu Glu Thr Gly Glu Asn Gln Met			
	100	105	110
tca aga ctg ggg gca gag gcc gtg gcc tag			366
Ser Arg Leu Gly Ala Glu Ala Val Ala *			
	115	120	

<210> 182

<211> 121

<212> PRT

<213> Homo sapiens

<400> 182

Met Ala Thr Pro Arg Gly Leu Gly Ala Leu Leu Leu Leu Leu Leu Leu			
1	5	10	15
Pro Thr Ser Gly Pro Gln Ala Pro Ser Leu Ser Leu Ser Gly Leu Ala			
	20	25	30
Gly Ser Pro Ser Glu Ser His Glu Asp Ala Trp Gly Gly Gly Thr Glu			
	35	40	45
Asn His Ser Glu Thr His Cys Ala Asn Gln Lys Ala Pro Arg Thr Val			
	50	55	60
Pro Ala Val Leu Arg Ser Ala Cys Pro Arg Phe Thr Asp Lys Glu Met			
65	70	75	80
Glu Gly Asp Arg Lys Gln Leu Lys Ala Ile His Gln Ala Ser Ser Gln			
	85	90	95
Gln Leu Leu Cys Val Asn Tyr Pro Glu Glu Thr Gly Glu Asn Gln Met			
	100	105	110
Ser Arg Leu Gly Ala Glu Ala Val Ala			
	115	120	

<210> 183

<211> 693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(693)

<400> 183

atg	gat	gat	tgt	gaa	gta	aat	gac	tta	cat	gaa	ggg	gca	gga	gtg	aaa	48
Met	Asp	Asp	Cys	Glu	Val	Asn	Asp	Leu	His	Glu	Gly	Ala	Gly	Val	Lys	
1				5					10					15		

cgg	tcc	ttc	ctg	atc	acc	ttg	gtg	tct	cct	ggg	gca	tta	gga	gcc	agg	96
Arg	Ser	Phe	Leu	Ile	Thr	Leu	Val	Ser	Pro	Gly	Ala	Leu	Gly	Ala	Arg	
			20					25					30			

tgt	gat	gta	aga	gaa	gga	gag	aga	ggg	ctt	gtg	aag	act	gag	cga	ggc	144
Cys	Asp	Val	Arg	Glu	Gly	Glu	Arg	Gly	Leu	Val	Lys	Thr	Glu	Arg	Gly	
		35					40					45				

ttg	gtg	aag	caa	ctc	gac	aag	aga	aac	gac	ctg	tgc	aaa	ggg	tgg	acc	192
Leu	Val	Lys	Gln	Leu	Asp	Lys	Arg	Asn	Asp	Leu	Cys	Lys	Gly	Trp	Thr	
	50					55					60					

aca	gcc	cac	aca	ggg	gtg	tgc	aaa	cac	acc	gct	cag	cct	gtc	agg	cat	240
Thr	Ala	His	Thr	Gly	Val	Cys	Lys	His	Thr	Ala	Gln	Pro	Val	Arg	His	
65					70					75					80	

att	tcc	tca	gag	acc	ctg	gca	cgg	cca	ggc	cct	cct	cac	ccc	aac	aat	288
Ile	Ser	Ser	Glu	Thr	Leu	Ala	Arg	Pro	Gly	Pro	Pro	His	Pro	Asn	Asn	
				85					90					95		

aca	gag	gag	tgg	ggg	ctg	gat	gca	ctt	agg	caa	gac	cta	aac	cac	agc	336
Thr	Glu	Glu	Trp	Gly	Leu	Asp	Ala	Leu	Arg	Gln	Asp	Leu	Asn	His	Ser	
			100					105					110			

agt	aag	aca	gca	gct	act	ccc	tgc	tgc	tac	atc	tgt	gga	caa	gca	ggg	384
Ser	Lys	Thr	Ala	Ala	Thr	Pro	Cys	Cys	Tyr	Ile	Cys	Gly	Gln	Ala	Gly	
		115					120					125				

cat	gaa	aat	gtg	tca	gac	agt	ggg	ggc	agc	tgg	att	cct	gat	tct	gtg	432
His	Glu	Asn	Val	Ser	Asp	Ser	Gly	Gly	Ser	Trp	Ile	Pro	Asp	Ser	Val	

130 135 140

att tta tca tca gct ttg aag tat gag gag gca gct gtg gct gcc ata 480
 Ile Leu Ser Ser Ala Leu Lys Tyr Glu Glu Ala Ala Val Ala Ala Ile
 145 150 155 160

ctg gga cca gga agc cag gtc agg aag ctg ctg ctg gcc ctg gca cag 528
 Leu Gly Pro Gly Ser Gln Val Arg Lys Leu Leu Leu Ala Leu Ala Gln
 165 170 175

gca gag gcc acc tca gca gaa gcc aca tca ctg cta gag agg cag cca 576
 Ala Glu Ala Thr Ser Ala Glu Ala Thr Ser Leu Leu Glu Arg Gln Pro
 180 185 190

gga aca ttc cag ctc ctc ctc act tgc ccc gct ggg gca atg cct gcc 624
 Gly Thr Phe Gln Leu Leu Leu Thr Cys Pro Ala Gly Ala Met Pro Ala
 195 200 205

act cct ctg ggt cgc tcc aga cag ctg gtg gcc aaa aag gct gtc act 672
 Thr Pro Leu Gly Arg Ser Arg Gln Leu Val Ala Lys Lys Ala Val Thr
 210 215 220

cac cat cgt ggt gaa cac tga 693
 His His Arg Gly Glu His *
 225 230

<210> 184
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 184

Met Asp Asp Cys Glu Val Asn Asp Leu His Glu Gly Ala Gly Val Lys
 1 5 10 15
 Arg Ser Phe Leu Ile Thr Leu Val Ser Pro Gly Ala Leu Gly Ala Arg
 20 25 30
 Cys Asp Val Arg Glu Gly Glu Arg Gly Leu Val Lys Thr Glu Arg Gly
 35 40 45
 Leu Val Lys Gln Leu Asp Lys Arg Asn Asp Leu Cys Lys Gly Trp Thr
 50 55 60
 Thr Ala His Thr Gly Val Cys Lys His Thr Ala Gln Pro Val Arg His
 65 70 75 80

Ile Ser Ser Glu Thr Leu Ala Arg Pro Gly Pro Pro His Pro Asn Asn
 85 90 95
 Thr Glu Glu Trp Gly Leu Asp Ala Leu Arg Gln Asp Leu Asn His Ser
 100 105 110
 Ser Lys Thr Ala Ala Thr Pro Cys Cys Tyr Ile Cys Gly Gln Ala Gly
 115 120 125
 His Glu Asn Val Ser Asp Ser Gly Gly Ser Trp Ile Pro Asp Ser Val
 130 135 140
 Ile Leu Ser Ser Ala Leu Lys Tyr Glu Glu Ala Ala Val Ala Ala Ile
 145 150 155 160
 Leu Gly Pro Gly Ser Gln Val Arg Lys Leu Leu Ala Leu Ala Gln
 165 170 175
 Ala Glu Ala Thr Ser Ala Glu Ala Thr Ser Leu Leu Glu Arg Gln Pro
 180 185 190
 Gly Thr Phe Gln Leu Leu Leu Thr Cys Pro Ala Gly Ala Met Pro Ala
 195 200 205
 Thr Pro Leu Gly Arg Ser Arg Gln Leu Val Ala Lys Lys Ala Val Thr
 210 215 220
 His His Arg Gly Glu His
 225 230

<210> 185
 <211> 1416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1416)

<400> 185

atg agg ctt ctc ctg gtg ctg ctg ctt ctg gct gct gtg tgt gct gcc	48
Met Arg Leu Leu Leu Val Leu Leu Leu Leu Ala Ala Val Cys Ala Ala	
1 5 10 15	
ctg gtt ggc cca tat gat gct gac ggt cag aca gca cct gct ggg agc	96
Leu Val Gly Pro Tyr Asp Ala Asp Gly Gln Thr Ala Pro Ala Gly Ser	
20 25 30	
tgg tca ctg ctc cca gga tct aat gag ggt gac ccc ttc att ccc atc	144
Trp Ser Leu Leu Pro Gly Ser Asn Glu Gly Asp Pro Phe Ile Pro Ile	
35 40 45	

aca gcc cga ggg ctt agg gat tac cag gat ccc tac gga gaa gtg gcg Thr Ala Arg Gly Leu Arg Asp Tyr Gln Asp Pro Tyr Gly Glu Val Ala 50 55 60	192
gta atg aca ccc cta cag aac acc tcc tac agg aca ccc cta cag aac Val Met Thr Pro Leu Gln Asn Thr Ser Tyr Arg Thr Pro Leu Gln Asn 65 70 75 80	240
acc tcc tat agg acc ccc cta cag gat act ccc tac agg gcg tcc cta Thr Ser Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Arg Ala Ser Leu 85 90 95	288
cag aac acc tcc tac agg ata ctc cct aca gga tac tcc cta cag gac Gln Asn Thr Ser Tyr Arg Ile Leu Pro Thr Gly Tyr Ser Leu Gln Asp 100 105 110	336
act ctc tac agg aca cca cta cag gac act ccc tac aga aaa ccc cta Thr Leu Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Arg Lys Pro Leu 115 120 125	384
cag gaa acc tcc tac agg aca ctc cct aca gga tac tcc cta cag aaa Gln Glu Thr Ser Tyr Arg Thr Leu Pro Thr Gly Tyr Ser Leu Gln Lys 130 135 140	432
acc cct aca gga aac ttc cta cag gac act ccc tac agg ata ctc cct Thr Pro Thr Gly Asn Phe Leu Gln Asp Thr Pro Tyr Arg Ile Leu Pro 145 150 155 160	480
aca gga tac tcc cta cag gaa acc ctc tac agg aca ctc cct aca gga Thr Gly Tyr Ser Leu Gln Glu Thr Leu Tyr Arg Thr Leu Pro Thr Gly 165 170 175	528
cat tct cta cag gat act ccc tac aag aaa acc cta caa gat act cct His Ser Leu Gln Asp Thr Pro Tyr Lys Lys Thr Leu Gln Asp Thr Pro 180 185 190	576
aca gaa aac ctc tac agg aca ctc cct aca gga cac tcc cta cag gaa Thr Glu Asn Leu Tyr Arg Thr Leu Pro Thr Gly His Ser Leu Gln Glu 195 200 205	624
acc tcc tac agg aca ccc cct aca gga cac cac cta cag gaa acc cct Thr Ser Tyr Arg Thr Pro Pro Thr Gly His His Leu Gln Glu Thr Pro 210 215 220	672

aca gga cac ccc tat atg aca ccc cta cag tac acc ccc tat agg aca	720
Thr Gly His Pro Tyr Met Thr Pro Leu Gln Tyr Thr Pro Tyr Arg Thr	
225 230 235 240	
cct gaa cag gac acc ccc tac agg acg ctc cct aca gga cac tcc cta	768
Pro Glu Gln Asp Thr Pro Tyr Arg Thr Leu Pro Thr Gly His Ser Leu	
245 250 255	
caa gac act ctt aca gga aac ctc tac agg aca ctc cct aca ggc tcc	816
Gln Asp Thr Leu Thr Gly Asn Leu Tyr Arg Thr Leu Pro Thr Gly Ser	
260 265 270	
cta cag gaa acc cct aca gga cct gcc tta cag gaa acc cct aca agg	864
Leu Gln Glu Thr Pro Thr Gly Pro Ala Leu Gln Glu Thr Pro Thr Arg	
275 280 285	
cgc tcc tac agg aaa cct cca cag gac act ccc tac aga aaa ccc cct	912
Arg Ser Tyr Arg Lys Pro Pro Gln Asp Thr Pro Tyr Arg Lys Pro Pro	
290 295 300	
aca gga cac tcc cta cag gac acc ccc tac agg aca ctc cct aca gga	960
Thr Gly His Ser Leu Gln Asp Thr Pro Tyr Arg Thr Leu Pro Thr Gly	
305 310 315 320	
cac ccc tac agg aca ccc cta ctg gac acc cct ata gga cac tgt aca	1008
His Pro Tyr Arg Thr Pro Leu Leu Asp Thr Pro Ile Gly His Cys Thr	
325 330 335	
gga cac ccc cta cag gac act ccc tac agg aaa ccc cta caa gac act	1056
Gly His Pro Leu Gln Asp Thr Pro Tyr Arg Lys Pro Leu Gln Asp Thr	
340 345 350	
cct aca gga aac ctc tac agg aca ctc cct aca gga aac ccc cta cgg	1104
Pro Thr Gly Asn Leu Tyr Arg Thr Leu Pro Thr Gly Asn Pro Leu Arg	
355 360 365	
gac act ccc tac agg gca ccc cct aca gga cac ccc tac agg acg atc	1152
Asp Thr Pro Tyr Arg Ala Pro Pro Thr Gly His Pro Tyr Arg Thr Ile	
370 375 380	
cct ata gga cac ctg tac agg ata tcc cct aca gga cac tcc cta cag	1200
Pro Ile Gly His Leu Tyr Arg Ile Ser Pro Thr Gly His Ser Leu Gln	

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<210> 186
<211> 471
<212> PRT
<213> Homo sapiens

<400> 186
Met Arg Leu Leu Leu Val Leu Leu Leu Leu Ala Ala Val Cys Ala Ala
 1          5          10          15
Leu Val Gly Pro Tyr Asp Ala Asp Gly Gln Thr Ala Pro Ala Gly Ser
          20          25          30
Trp Ser Leu Leu Pro Gly Ser Asn Glu Gly Asp Pro Phe Ile Pro Ile
          35          40          45
Thr Ala Arg Gly Leu Arg Asp Tyr Gln Asp Pro Tyr Gly Glu Val Ala
          50          55          60
Val Met Thr Pro Leu Gln Asn Thr Ser Tyr Arg Thr Pro Leu Gln Asn
65          70          75          80
Thr Ser Tyr Arg Thr Pro Leu Gln Asp Thr Pro Tyr Arg Ala Ser Leu
          85          90          95
Gln Asn Thr Ser Tyr Arg Ile Leu Pro Thr Gly Tyr Ser Leu Gln Asp
          100          105          110

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450 455 460
 Pro Pro Thr Gly Tyr Pro Leu
 465 470

<210> 187
 <211> 525
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(525)

<400> 187

atg aag acg ctg tgg ctc ctt ctg tct ctt gct ctg ttt atc ttt cct 48
 Met Lys Thr Leu Trp Leu Leu Leu Ser Leu Ala Leu Phe Ile Phe Pro
 1 5 10 15

ttc ttg gcg gtg tgt tct gga agt ggc tgc atc cct gac tct gtg gtg 96
 Phe Leu Ala Val Cys Ser Gly Ser Gly Cys Ile Pro Asp Ser Val Val
 20 25 30

gag tgt ccg gaa ggg gct gtc tgc ccc aca gct gca gct ccc gag gca 144
 Glu Cys Pro Glu Gly Ala Val Cys Pro Thr Ala Ala Ala Pro Glu Ala
 35 40 45

ccc gcc cct cca cca tgc tca cag gtc cct ttc atc ccc tcc agc cct 192
 Pro Ala Pro Pro Pro Cys Ser Gln Val Pro Phe Ile Pro Ser Ser Pro
 50 55 60

agg agt gct cta tcc aaa gaa gtc tgg cca att gga tgc agt aca tct 240
 Arg Ser Ala Leu Ser Lys Glu Val Trp Pro Ile Gly Cys Ser Thr Ser
 65 70 75 80

ttt ggt atg cag aag gtg aat ctc ata att ggt tct att ttt cca gtg 288
 Phe Gly Met Gln Lys Val Asn Leu Ile Ile Gly Ser Ile Phe Pro Val
 85 90 95

tct gca ttc ctc ctg aag gat gaa gat aac tgc tgt gtc cct ttc ctg 336
 Ser Ala Phe Leu Leu Lys Asp Glu Asp Asn Cys Cys Val Pro Phe Leu
 100 105 110

ctc aat gaa act ctg caa atc cta cga agc cct ttt acc aca tgg gga 384
 Leu Asn Glu Thr Leu Gln Ile Leu Arg Ser Pro Phe Thr Thr Trp Gly

<210> 188
<211> 174
<212> PRT
<213> Homo sapiens

<400> 188

Met	Lys	Thr	Leu	Trp	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Phe	Ile	Phe	Pro
1			5					10					15		
Phe	Leu	Ala	Val	Cys	Ser	Gly	Ser	Gly	Cys	Ile	Pro	Asp	Ser	Val	Val
			20					25					30		
Glu	Cys	Pro	Glu	Gly	Ala	Val	Cys	Pro	Thr	Ala	Ala	Ala	Pro	Glu	Ala
		35					40					45			
Pro	Ala	Pro	Pro	Pro	Cys	Ser	Gln	Val	Pro	Phe	Ile	Pro	Ser	Ser	Pro
	50					55					60				
Arg	Ser	Ala	Leu	Ser	Lys	Glu	Val	Trp	Pro	Ile	Gly	Cys	Ser	Thr	Ser
65					70					75					80
Phe	Gly	Met	Gln	Lys	Val	Asn	Leu	Ile	Ile	Gly	Ser	Ile	Phe	Pro	Val
			85						90					95	
Ser	Ala	Phe	Leu	Leu	Lys	Asp	Glu	Asp	Asn	Cys	Cys	Val	Pro	Phe	Leu
			100					105					110		
Leu	Asn	Glu	Thr	Leu	Gln	Ile	Leu	Arg	Ser	Pro	Phe	Thr	Thr	Trp	Gly
		115					120					125			
Phe	Gly	Lys	Leu	Ser	Gly	Leu	Ala	Lys	Tyr	Trp	Ser	Leu	Glu	Ser	Arg
	130					135					140				
Arg	Gln	Ser	Arg	Asn	Ala	Leu	Leu	Ala	Gly	Cys	His	Met	Ala	Pro	Glu
145					150					155					160
Leu	Cys	Ser	Thr	Val	Glu	Trp	Gln	Ser	Asp	Glu	Ala	Asp	Val		
				165					170						

<400> 188															
Met	Lys	Thr	Leu	Trp	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Phe	Ile	Phe	Pro
1				5					10					15	
Phe	Leu	Ala	Val	Cys	Ser	Gly	Ser	Gly	Cys	Ile	Pro	Asp	Ser	Val	Val
			20					25					30		
Glu	Cys	Pro	Glu	Gly	Ala	Val	Cys	Pro	Thr	Ala	Ala	Ala	Pro	Glu	Ala
		35					40					45			
Pro	Ala	Pro	Pro	Pro	Cys	Ser	Gln	Val	Pro	Phe	Ile	Pro	Ser	Ser	Pro
	50					55					60				
Arg	Ser	Ala	Leu	Ser	Lys	Glu	Val	Trp	Pro	Ile	Gly	Cys	Ser	Thr	Ser
65					70					75					80
Phe	Gly	Met	Gln	Lys	Val	Asn	Leu	Ile	Ile	Gly	Ser	Ile	Phe	Pro	Val
			85						90					95	
Ser	Ala	Phe	Leu	Leu	Lys	Asp	Glu	Asp	Asn	Cys	Cys	Val	Pro	Phe	Leu
			100					105					110		
Leu	Asn	Glu	Thr	Leu	Gln	Ile	Leu	Arg	Ser	Pro	Phe	Thr	Thr	Trp	Gly
		115					120					125			
Phe	Gly	Lys	Leu	Ser	Gly	Leu	Ala	Lys	Tyr	Trp	Ser	Leu	Glu	Ser	Arg
	130					135					140				
Arg	Gln	Ser	Arg	Asn	Ala	Leu	Leu	Ala	Gly	Cys	His	Met	Ala	Pro	Glu
145					150					155					160
Leu	Cys	Ser	Thr	Val	Glu	Trp	Gln	Ser	Asp	Glu	Ala	Asp	Val		
				165					170						

<210> 189
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(432)

<400> 189

atg gcc ccg ccg ctc ctg ctg ctg ctg ctg gcc agt gga gcg gcc gcc	48
Met Ala Pro Pro Leu Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala	
1 5 10 15	
tgc ccg ctg ccc tgc gtc tgc cag aac ctg tcc gag tcg ctc agc acc	96
Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr	
20 25 30	
ctc tgt gcc cac cga ggc ctg ctg ttt gtg ccg ccc aac gtg gac cgg	144
Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg	
35 40 45	
cgc aca gtg gag ctg cgg ctg gct gac aac ttc atc cag gcc ctg ggg	192
Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly	
50 55 60	
ccc cct gac ttc cgc aac atg acg gga ctg gtg gac ctg aca ctg tct	240
Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser	
65 70 75 80	
cgc aat gcc atc acc cgc att ggg gcc cgc gcc ttt ggg gac ctc gag	288
Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu	
85 90 95	
agc ctg cgt tcc ctc cac ctt gac ggc aac agg ctg gtg gag ctg ggc	336
Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly	
100 105 110	
acc ggg agc ctc cgg ggc ccc gtc aat ctg cag cac ctc atc ctc agc	384
Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser	
115 120 125	

ggc aac cag ctg ggc gca tcg cgc cgg gag cct tcg acg act tcc tag 432
 Gly Asn Gln Leu Gly Ala Ser Arg Arg Glu Pro Ser Thr Thr Ser *
 130 135 140

<210> 190
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Ala Pro Pro Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala
 1 5 10 15
 Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr
 20 25 30
 Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg
 35 40 45
 Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly
 50 55 60
 Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser
 65 70 75 80
 Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu
 85 90 95
 Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly
 100 105 110
 Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser
 115 120 125
 Gly Asn Gln Leu Gly Ala Ser Arg Arg Glu Pro Ser Thr Thr Ser
 130 135 140

<210> 191
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(357)

<400> 191
 atg ggt gta ggc aca gca tcc gtc cta aag aac tgt ctc ttc ctg ggc 48
 Met Gly Val Gly Thr Ala Ser Val Leu Lys Asn Cys Leu Phe Leu Gly
 1 5 10 15

cct ctg gct tgg gct ctc ctg gtc ccc gga gga ctc cag gcg gga agg 96
 Pro Leu Ala Trp Ala Leu Leu Val Pro Gly Gly Leu Gln Ala Gly Arg
 20 25 30

aca ccg ggg gtc tcc ctg gtt aca cca ggc ata ggg ggg gag gac acc 144
 Thr Pro Gly Val Ser Leu Val Thr Pro Gly Ile Gly Gly Glu Asp Thr
 35 40 45

ctt cgg ggg gaa acc cgt ttt tcg cgc cgg tat ttt ttc ggc gat cat 192
 Leu Arg Gly Glu Thr Arg Phe Ser Arg Arg Tyr Phe Phe Gly Asp His
 50 55 60

cat cga gcc ttg gcc cac tgg gac aaa ctt act agt ttt acg gat ctt 240
 His Arg Ala Leu Ala His Trp Asp Lys Leu Thr Ser Phe Thr Asp Leu
 65 70 75 80

cag acc cgg gta aac ggg aga ctt tgc acg ctt atc agc gcc ctg atg 288
 Gln Thr Arg Val Asn Gly Arg Leu Cys Thr Leu Ile Ser Ala Leu Met
 85 90 95

ttc atg gtt tta cct cat tca aat aaa gtg ata agt aag ttc att cga 336
 Phe Met Val Leu Pro His Ser Asn Lys Val Ile Ser Lys Phe Ile Arg
 100 105 110

gag ggt ttc aag caa aaa taa 357
 Glu Gly Phe Lys Gln Lys *
 115

<210> 192

<211> 118

<212> PRT

<213> Homo sapiens

<400> 192

Met Gly Val Gly Thr Ala Ser Val Leu Lys Asn Cys Leu Phe Leu Gly
 1 5 10 15

Pro Leu Ala Trp Ala Leu Leu Val Pro Gly Gly Leu Gln Ala Gly Arg
 20 25 30

Thr Pro Gly Val Ser Leu Val Thr Pro Gly Ile Gly Gly Glu Asp Thr
 35 40 45

Leu Arg Gly Glu Thr Arg Phe Ser Arg Arg Tyr Phe Phe Gly Asp His

50 55 60
 His Arg Ala Leu Ala His Trp Asp Lys Leu Thr Ser Phe Thr Asp Leu
 65 70 75 80
 Gln Thr Arg Val Asn Gly Arg Leu Cys Thr Leu Ile Ser Ala Leu Met
 85 90 95
 Phe Met Val Leu Pro His Ser Asn Lys Val Ile Ser Lys Phe Ile Arg
 100 105 110
 Glu Gly Phe Lys Gln Lys
 115

<210> 193
 <211> 324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(324)

<400> 193
 atg gtt ctc aaa gtg ccg acg tcc aaa gtc ctg cta gtc ctg gcc acc 48
 Met Val Leu Lys Val Pro Thr Ser Lys Val Leu Leu Val Leu Ala Thr
 1 5 10 15

 ttg ttc gcc gtg gcg gcg atg atc agc agc tgg atg ccc cag gtg gcg 96
 Leu Phe Ala Val Ala Ala Met Ile Ser Ser Trp Met Pro Gln Val Ala
 20 25 30

 gcc agt ccg ctc gca ccc acg gaa tac gaa cag aga cgc atg atg tgc 144
 Ala Ser Pro Leu Ala Pro Thr Glu Tyr Glu Gln Arg Arg Met Met Cys
 35 40 45

 tcc acc ggc ctc agc gat gtg ata cag aag ata tgc gta agc gga acg 192
 Ser Thr Gly Leu Ser Asp Val Ile Gln Lys Ile Cys Val Ser Gly Thr
 50 55 60

 gtg gcc ctt ggc gat gta ttt ccc aac agt ttc ggg aag cgc agg aag 240
 Val Ala Leu Gly Asp Val Phe Pro Asn Ser Phe Gly Lys Arg Arg Lys
 65 70 75 80

 cgc gac ttg cag aac gta acc gat ttg tgc tgc aag tcg ggt ggc tgc 288
 Arg Asp Leu Gln Asn Val Thr Asp Leu Cys Cys Lys Ser Gly Gly Cys
 85 90 95

	20	25	30	
tcc cag cgc ctg cac ctg ctc ctg gag acg ctc acc ttc ccg gct gtt				144
Ser Gln Arg Leu His Leu Leu Leu Glu Thr Leu Thr Phe Pro Ala Val				
	35	40	45	
gcc cta att ctg caa cgt gtc aaa gga caa atg tca cat gtc atg tct				192
Ala Leu Ile Leu Gln Arg Val Lys Gly Gln Met Ser His Val Met Ser				
	50	55	60	
tcc ctg ccc tgg gac agc cgc ctc tac ctg gca ctc atc tct ggc tcc				240
Ser Leu Pro Trp Asp Ser Arg Leu Tyr Leu Ala Leu Ile Ser Gly Ser				
	65	70	75	80
tcg gcg tgg atc agt tac tac atg atc atg ctg tgg agc att tca ctg				288
Ser Ala Trp Ile Ser Tyr Tyr Met Ile Met Leu Trp Ser Ile Ser Leu				
		85	90	95
agt ttc ttc tgg gtg cct gga ttt tgt gac cgt ttg gtg gcc ttt aag				336
Ser Phe Phe Trp Val Pro Gly Phe Cys Asp Arg Leu Val Ala Phe Lys				
	100	105	110	
aag aga ctt tat gag agt cag ttt tgc cag tac acc tct gga tat aaa				384
Lys Arg Leu Tyr Glu Ser Gln Phe Cys Gln Tyr Thr Ser Gly Tyr Lys				
	115	120	125	
gaa aat caa aat ata agt ttt gtc aac aag aac tac tta tta tac aac				432
Glu Asn Gln Asn Ile Ser Phe Val Asn Lys Asn Tyr Leu Leu Tyr Asn				
	130	135	140	
tac att ggg gct ttt tgc att ttg gct gtg ctg act tat gga agc agg				480
Tyr Ile Gly Ala Phe Cys Ile Leu Ala Val Leu Thr Tyr Gly Ser Arg				
	145	150	155	160
cat aca ctg ggt gtg tga				498
His Thr Leu Gly Val *				
	165			

<210> 196

<211> 165

<212> PRT

<213> Homo sapiens

<400> 196

Met	Arg	Glu	Ala	Gly	Gly	Leu	Lys	Asp	Thr	Thr	Gly	Lys	Leu	Trp	Lys
1				5					10					15	
Ser	Phe	Leu	Leu	Pro	Arg	Ala	Leu	Leu	Pro	Ser	Gly	Ala	Arg	Ala	Ala
		20						25					30		
Ser	Gln	Arg	Leu	His	Leu	Leu	Leu	Glu	Thr	Leu	Thr	Phe	Pro	Ala	Val
	35						40					45			
Ala	Leu	Ile	Leu	Gln	Arg	Val	Lys	Gly	Gln	Met	Ser	His	Val	Met	Ser
50						55					60				
Ser	Leu	Pro	Trp	Asp	Ser	Arg	Leu	Tyr	Leu	Ala	Leu	Ile	Ser	Gly	Ser
65					70					75				80	
Ser	Ala	Trp	Ile	Ser	Tyr	Tyr	Met	Ile	Met	Leu	Trp	Ser	Ile	Ser	Leu
				85					90					95	
Ser	Phe	Phe	Trp	Val	Pro	Gly	Phe	Cys	Asp	Arg	Leu	Val	Ala	Phe	Lys
		100						105					110		
Lys	Arg	Leu	Tyr	Glu	Ser	Gln	Phe	Cys	Gln	Tyr	Thr	Ser	Gly	Tyr	Lys
	115					120							125		
Glu	Asn	Gln	Asn	Ile	Ser	Phe	Val	Asn	Lys	Asn	Tyr	Leu	Leu	Tyr	Asn
	130					135					140				
Tyr	Ile	Gly	Ala	Phe	Cys	Ile	Leu	Ala	Val	Leu	Thr	Tyr	Gly	Ser	Arg
145					150					155					160
His	Thr	Leu	Gly	Val											
				165											

<210> 197
 <211> 573
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(573)

<400> 197

atg	ctg	ggc	ctc	ctg	ggg	agc	aca	gcc	ctc	gtg	gga	tgg	atc	aca	ggt	48
Met	Leu	Gly	Leu	Leu	Gly	Ser	Thr	Ala	Leu	Val	Gly	Trp	Ile	Thr	Gly	
1				5					10					15		
gct	gct	gtg	gcg	gtc	ctg	ctg	ctg	ctg	ctg	ctg	ctg	gcc	acc	tgc	ctt	96
Ala	Ala	Val	Ala	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Thr	Cys	Leu	
			20					25					30			

ttc cac gga cgg cag gac tgt gac gtg gag agg aac cgt aca gct gca	144
Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg Thr Ala Ala	
35 40 45	
ggg gga aac cga gtc cgc cgg gcc cag cct tgg ccc ttc cgg cgg cgg	192
Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro Phe Arg Arg Arg	
50 55 60	
ggc cac ctg gga atc ttt cac cat cac cgt cat cct ggc cac gag acg	240
Gly His Leu Gly Ile Phe His His His Arg His Pro Gly His Glu Thr	
65 70 75 80	
gaa gga gag ccg ccg gag gag cac ggg gca cct gcg atc gcg aag agc	288
Glu Gly Glu Pro Pro Glu Glu His Gly Ala Pro Ala Ile Ala Lys Ser	
85 90 95	
ctc ctg ttc tgg atg gga gcg aag gct ccg aga gga cct aag gtt gct	336
Leu Leu Phe Trp Met Gly Ala Lys Ala Pro Arg Gly Pro Lys Val Ala	
100 105 110	
cag tgg gcc atg gaa acg gca gtg att ggg gtg gtg gtg gtg ctg ttc	384
Gln Trp Ala Met Glu Thr Ala Val Ile Gly Val Val Val Val Leu Phe	
115 120 125	
gtg gtg act gtg gcc atc acc tgc gtc ctc tgc tgc ttc agc tgt gac	432
Val Val Thr Val Ala Ile Thr Cys Val Leu Cys Cys Phe Ser Cys Asp	
130 135 140	
tca agg gcc cag gat cct cag ggg ggt cct ggc cgc agc ttc acg gtg	480
Ser Arg Ala Gln Asp Pro Gln Gly Gly Pro Gly Arg Ser Phe Thr Val	
145 150 155 160	
gcc acg ttt cgc cag gaa gct tct ctc ttc acg ggg cct gtt cgc cat	528
Ala Thr Phe Arg Gln Glu Ala Ser Leu Phe Thr Gly Pro Val Arg His	
165 170 175	
gcc cag cca gtg cca agt gcc cag gac ttc tgg acc ttc atg tga	573
Ala Gln Pro Val Pro Ser Ala Gln Asp Phe Trp Thr Phe Met *	
180 185 190	

<210> 198

<211> 190

<213> Homo sapiens

Met	Leu	Gly	Leu	Leu	Gly	Ser	Thr	Ala	Leu	Val	Gly	Trp	Ile	Thr	Gly
1				5					10					15	
Ala	Ala	Val	Ala	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Thr	Cys	Leu
			20					25					30		
Phe	His	Gly	Arg	Gln	Asp	Cys	Asp	Val	Glu	Arg	Asn	Arg	Thr	Ala	Ala
		35					40					45			
Gly	Gly	Asn	Arg	Val	Arg	Arg	Ala	Gln	Pro	Trp	Pro	Phe	Arg	Arg	Arg
	50					55					60				
Gly	His	Leu	Gly	Ile	Phe	His	His	His	Arg	His	Pro	Gly	His	Glu	Thr
65					70					75					80
Glu	Gly	Glu	Pro	Pro	Glu	Glu	His	Gly	Ala	Pro	Ala	Ile	Ala	Lys	Ser
				85					90					95	
Leu	Leu	Phe	Trp	Met	Gly	Ala	Lys	Ala	Pro	Arg	Gly	Pro	Lys	Val	Ala
			100					105					110		
Gln	Trp	Ala	Met	Glu	Thr	Ala	Val	Ile	Gly	Val	Val	Val	Val	Leu	Phe
		115					120					125			
Val	Val	Thr	Val	Ala	Ile	Thr	Cys	Val	Leu	Cys	Cys	Phe	Ser	Cys	Asp
	130					135					140				
Ser	Arg	Ala	Gln	Asp	Pro	Gln	Gly	Gly	Pro	Gly	Arg	Ser	Phe	Thr	Val
145					150					155					160
Ala	Thr	Phe	Arg	Gln	Glu	Ala	Ser	Leu	Phe	Thr	Gly	Pro	Val	Arg	His
				165					170					175	
Ala	Gln	Pro	Val	Pro	Ser	Ala	Gln	Asp	Phe	Trp	Thr	Phe	Met		
			180					185					190		

<211> 489

<213> Homo sapiens

<221> CDS

<222> (1)...(489)

atg gcg ctg cct cca ggc cca gcc gcc ctc cgg cac aca ctg ctg ctc
Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu
1 5 10 15

<212> PRT

<213> Homo sapiens

<400> 200

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Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu
 1          5          10          15
Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu Glu Pro Gln Ile
          20          25          30
Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn Glu Arg His
          35          40          45
Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr Pro Arg Leu Ala
          50          55          60
Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser Arg Leu Leu
65          70          75          80
Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr Phe Thr Val
          85          90          95
Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu Gln Asp Pro
          100          105          110
Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu Asn Val Gln Cys
          115          120          125
Arg Glu Tyr Leu Leu Val Val Leu Phe Ala Leu Asp Arg Ala Asn Pro
          130          135          140
Pro Ala Asn Val Thr Arg Asp Arg Pro Cys Leu Pro Ser Asp Cys Val
145          150          155          160
His Leu

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<210> 201

<211> 1113

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1113)

<400> 201

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atg aga act aaa acc cag caa cta aga ttt agg caa aga aaa cag att      48
Met Arg Thr Lys Thr Gln Gln Leu Arg Phe Arg Gln Arg Lys Gln Ile
 1          5          10          15

cca gaa tca gca cag agc ctg ctg ctg ctg ctg ctt ctg tct gct      96
Pro Glu Ser Ala Gln Ser Leu Leu Leu Leu Leu Leu Leu Ser Ala

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20	25	30	
gct tct gct gct gga ggc att gct aac aca ctc acc caa gcc tta gct Ala Ser Ala Ala Gly Gly Ile Ala Asn Thr Leu Thr Gln Ala Leu Ala 35 40 45			144
ctt aat aga gac atg ttt gca gct gaa tgc ccc agt gct tgt ggt tta Leu Asn Arg Asp Met Phe Ala Ala Glu Cys Pro Ser Ala Cys Gly Leu 50 55 60			192
agc aaa att gtt aac act gtg cga agt tca tgg cct tct gcc aat gcc Ser Lys Ile Val Asn Thr Val Arg Ser Ser Trp Pro Ser Ala Asn Ala 65 70 75 80			240
att gta cag tcc ctg aga gaa aaa agg aga aag ctc ctt ggg ata ata Ile Val Gln Ser Leu Arg Glu Lys Arg Arg Lys Leu Leu Gly Ile Ile 85 90 95			288
agg cag gtg att ctc aga ccc ctc agt gga gtt tgt ggg tgg cgg cag Arg Gln Val Ile Leu Arg Pro Leu Ser Gly Val Cys Gly Trp Arg Gln 100 105 110			336
cag tgg tgg tta gtg agg aaa gcc cgt ctt cag ggt atg tgc aaa tgc Gln Trp Trp Leu Val Arg Lys Ala Arg Leu Gln Gly Met Cys Lys Cys 115 120 125			384
acc aca gct ttg ctg ctg ggg gag ggt ggg gtt gct att agt ggc agc Thr Thr Ala Leu Leu Leu Gly Glu Gly Gly Val Ala Ile Ser Gly Ser 130 135 140			432
agc tgc cgt cag ttg gct ctt agg ctc tgg gga gca tgt gct ttg ggc Ser Cys Arg Gln Leu Ala Leu Arg Leu Trp Gly Ala Cys Ala Leu Gly 145 150 155 160			480
ctt ggt ggt ggc tat cat ggt gtc agt ggt agc agt ggg gag tgg cag Leu Gly Gly Gly Tyr His Gly Val Ser Gly Ser Ser Gly Glu Trp Gln 165 170 175			528
cag cag gga gag cca gtt ctc agg cgc gcg ctc aaa tgc ctg tgc ttg Gln Gln Gly Glu Pro Val Leu Arg Arg Ala Leu Lys Cys Leu Cys Leu 180 185 190			576
cgt tta gga agc gac gag aat ggg tgg ggt caa cac aat act act gct			624

Arg	Leu	Gly	Ser	Asp	Glu	Asn	Gly	Trp	Gly	Gln	His	Asn	Thr	Thr	Ala		
	195						200					205					
gcc	cgc	tca	agg	ttg	aca	gag	tta	aat	gat	ttg	cag	gga	cca	ggc	act	672	
Ala	Arg	Ser	Arg	Leu	Thr	Glu	Leu	Asn	Asp	Leu	Gln	Gly	Pro	Gly	Thr		
	210					215				220							
gtg	ggg	ggc	gta	tgg	ctg	ttt	tct	ctg	gcc	tcg	aaa	acc	att	ttc	tcc	720	
Val	Gly	Gly	Val	Trp	Leu	Phe	Ser	Leu	Ala	Ser	Lys	Thr	Ile	Phe	Ser		
	225				230				235						240		
aga	gcc	gaa	cta	cgc	tct	aag	cac	cgg	aac	tac	ctt	att	agg	gat	aaa	768	
Arg	Ala	Glu	Leu	Arg	Ser	Lys	His	Arg	Asn	Tyr	Leu	Ile	Arg	Asp	Lys		
			245					250						255			
tct	cgg	tct	agg	atc	tcg	cca	gaa	tct	cgt	gaa	cta	gtg	cta	agg	cac	816	
Ser	Arg	Ser	Arg	Ile	Ser	Pro	Glu	Ser	Arg	Glu	Leu	Val	Leu	Arg	His		
			260				265					270					
aga	acc	cat	ttt	ggc	aca	gaa	aca	tac	tac	ttg	agg	tcg	aga	att	cta	864	
Arg	Thr	His	Phe	Gly	Thr	Glu	Thr	Tyr	Tyr	Leu	Arg	Ser	Arg	Ile	Leu		
		275				280						285					
agg	ggc	aag	ctg	acc	ctc	cat	gtg	ata	ccc	ggt	gcg	gct	gtc	aga	cag	912	
Arg	Gly	Lys	Leu	Thr	Leu	His	Val	Ile	Pro	Val	Ala	Ala	Val	Arg	Gln		
	290					295				300							
tat	ctt	acc	aca	agc	gac	ctt	cta	aat	agc	ggt	ttt	cta	tat	gat	gct	960	
Tyr	Leu	Thr	Thr	Ser	Asp	Leu	Leu	Asn	Ser	Val	Phe	Leu	Tyr	Asp	Ala		
	305				310				315						320		
ggc	ggc	agc	cca	gtg	agg	gaa	gtg	caa	caa	gta	tgg	ttc	tcc	tgc	ttg	1008	
Gly	Gly	Ser	Pro	Val	Arg	Glu	Val	Gln	Gln	Val	Trp	Phe	Ser	Cys	Leu		
			325					330						335			
tca	act	gtg	gaa	aca	gcg	acc	ctg	aaa	gtg	gag	gag	cca	cag	ctg	gaa	1056	
Ser	Thr	Val	Glu	Thr	Ala	Thr	Leu	Lys	Val	Glu	Glu	Pro	Gln	Leu	Glu		
			340				345						350				
tcg	tgt	ccg	tct	gaa	tac	acg	cac	ctt	tcc	tat	gag	cct	tgt	aaa	gcc	1104	
Ser	Cys	Pro	Ser	Glu	Tyr	Thr	His	Leu	Ser	Tyr	Glu	Pro	Cys	Lys	Ala		
		355					360					365					

agt cgt tga
 Ser Arg *
 370

1113

<210> 202
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 202

Met	Arg	Thr	Lys	Thr	Gln	Gln	Leu	Arg	Phe	Arg	Gln	Arg	Lys	Gln	Ile
1				5					10					15	
Pro	Glu	Ser	Ala	Gln	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Ala
			20					25					30		
Ala	Ser	Ala	Ala	Gly	Gly	Ile	Ala	Asn	Thr	Leu	Thr	Gln	Ala	Leu	Ala
		35					40					45			
Leu	Asn	Arg	Asp	Met	Phe	Ala	Ala	Glu	Cys	Pro	Ser	Ala	Cys	Gly	Leu
	50					55					60				
Ser	Lys	Ile	Val	Asn	Thr	Val	Arg	Ser	Ser	Trp	Pro	Ser	Ala	Asn	Ala
65				70					75					80	
Ile	Val	Gln	Ser	Leu	Arg	Glu	Lys	Arg	Arg	Lys	Leu	Leu	Gly	Ile	Ile
			85					90						95	
Arg	Gln	Val	Ile	Leu	Arg	Pro	Leu	Ser	Gly	Val	Cys	Gly	Trp	Arg	Gln
		100					105						110		
Gln	Trp	Trp	Leu	Val	Arg	Lys	Ala	Arg	Leu	Gln	Gly	Met	Cys	Lys	Cys
	115					120						125			
Thr	Thr	Ala	Leu	Leu	Leu	Gly	Glu	Gly	Gly	Val	Ala	Ile	Ser	Gly	Ser
	130					135					140				
Ser	Cys	Arg	Gln	Leu	Ala	Leu	Arg	Leu	Trp	Gly	Ala	Cys	Ala	Leu	Gly
145				150					155					160	
Leu	Gly	Gly	Gly	Tyr	His	Gly	Val	Ser	Gly	Ser	Ser	Gly	Glu	Trp	Gln
			165					170						175	
Gln	Gln	Gly	Glu	Pro	Val	Leu	Arg	Arg	Ala	Leu	Lys	Cys	Leu	Cys	Leu
		180					185					190			
Arg	Leu	Gly	Ser	Asp	Glu	Asn	Gly	Trp	Gly	Gln	His	Asn	Thr	Thr	Ala
	195					200						205			
Ala	Arg	Ser	Arg	Leu	Thr	Glu	Leu	Asn	Asp	Leu	Gln	Gly	Pro	Gly	Thr
	210				215					220					
Val	Gly	Gly	Val	Trp	Leu	Phe	Ser	Leu	Ala	Ser	Lys	Thr	Ile	Phe	Ser
225				230					235					240	
Arg	Ala	Glu	Leu	Arg	Ser	Lys	His	Arg	Asn	Tyr	Leu	Ile	Arg	Asp	Lys
			245					250						255	

"08290" 2226860

Ser Arg Ser Arg Ile Ser Pro Glu Ser Arg Glu Leu Val Leu Arg His
 260 265 270
 Arg Thr His Phe Gly Thr Glu Thr Tyr Tyr Leu Arg Ser Arg Ile Leu
 275 280 285
 Arg Gly Lys Leu Thr Leu His Val Ile Pro Val Ala Ala Val Arg Gln
 290 295 300
 Tyr Leu Thr Thr Ser Asp Leu Leu Asn Ser Val Phe Leu Tyr Asp Ala
 305 310 315 320
 Gly Gly Ser Pro Val Arg Glu Val Gln Gln Val Trp Phe Ser Cys Leu
 325 330 335
 Ser Thr Val Glu Thr Ala Thr Leu Lys Val Glu Glu Pro Gln Leu Glu
 340 345 350
 Ser Cys Pro Ser Glu Tyr Thr His Leu Ser Tyr Glu Pro Cys Lys Ala
 355 360 365
 Ser Arg
 370

<210> 203
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(279)

<400> 203

atg gag ttg tgg tgg gag tgg gca ttg ctg gcc act ctc ctg gtg ctt 48
 Met Glu Leu Trp Trp Glu Trp Ala Leu Leu Ala Thr Leu Leu Val Leu
 1 5 10 15

gtt gca ggg agc cag aaa ata tgt cag agt ata gag gac ccc cca tac 96
 Val Ala Gly Ser Gln Lys Ile Cys Gln Ser Ile Glu Asp Pro Pro Tyr
 20 25 30

aat tta aag aat aag gag gag gag gag gag aag gag gag gag gga gag 144
 Asn Leu Lys Asn Lys Glu Glu Glu Glu Glu Lys Glu Glu Glu Gly Glu
 35 40 45

gag aag gta gaa cat aac gtt tcc atc cag gtt aag aaa cag cca ggc 192
 Glu Lys Val Glu His Asn Val Ser Ile Gln Val Lys Lys Gln Pro Gly
 50 55 60

205

ctt ggt ctt ctg ctc ctg gac atc ccg gcc ttc act gac cac cgt ctg 240
 Leu Gly Leu Leu Leu Leu Asp Ile Pro Ala Phe Thr Asp His Arg Leu
 65 70 75 80

aac agg tcc gag ccc tgc tct acc ctg tgc ttt gct tga 279
 Asn Arg Ser Glu Pro Cys Ser Thr Leu Cys Phe Ala *
 85 90

<210> 204
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 204
 Met Glu Leu Trp Trp Glu Trp Ala Leu Leu Ala Thr Leu Leu Val Leu
 1 5 10 15
 Val Ala Gly Ser Gln Lys Ile Cys Gln Ser Ile Glu Asp Pro Pro Tyr
 20 25 30
 Asn Leu Lys Asn Lys Glu Glu Glu Glu Lys Glu Glu Glu Gly Glu
 35 40 45
 Glu Lys Val Glu His Asn Val Ser Ile Gln Val Lys Lys Gln Pro Gly
 50 55 60
 Leu Gly Leu Leu Leu Leu Asp Ile Pro Ala Phe Thr Asp His Arg Leu
 65 70 75 80
 Asn Arg Ser Glu Pro Cys Ser Thr Leu Cys Phe Ala
 85 90

<210> 205
 <211> 657
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(657)

<400> 205
 atg cga gac aaa gca gcc cct gcc tgg aca gtg ctg gcc ctg atg caa 48
 Met Arg Asp Lys Ala Ala Pro Ala Trp Thr Val Leu Ala Leu Met Gln
 1 5 10 15

ggg gtg cag gca aag aag gag agg ccc tct tgg ctt cgg gat gca gtt 96

CCDS:22669.1

Gly	Val	Gln	Ala	Lys	Lys	Glu	Arg	Pro	Ser	Trp	Leu	Arg	Asp	Ala	Val	
			20					25					30			
ctc	tgc	tcc	acc	aca	cca	gtg	ccc	agg	gcc	ttt	ccc	atg	gca	aag	cac	144
Leu	Cys	Ser	Thr	Thr	Pro	Val	Pro	Arg	Ala	Phe	Pro	Met	Ala	Lys	His	
		35					40					45				
caa	cac	ctg	ccc	tta	ttt	aaa	agc	tta	tct	gta	gcc	cag	cag	aaa	aca	192
Gln	His	Leu	Pro	Leu	Phe	Lys	Ser	Leu	Ser	Val	Ala	Gln	Gln	Lys	Thr	
	50					55					60					
agg	cac	gac	aca	tat	ttg	agg	ttt	aac	atc	ttg	att	ctc	agg	ctt	tat	240
Arg	His	Asp	Thr	Tyr	Leu	Arg	Phe	Asn	Ile	Leu	Ile	Leu	Arg	Leu	Tyr	
65				70						75					80	
aac	act	gga	tat	tat	tgg	caa	cac	cat	gaa	aca	aag	aaa	cag	aag	ctt	288
Asn	Thr	Gly	Tyr	Tyr	Trp	Gln	His	His	Glu	Thr	Lys	Lys	Gln	Lys	Leu	
			85					90						95		
ctg	ccc	act	cct	cca	cat	gtg	aca	tta	gga	att	cag	tgt	agg	aca	gtg	336
Leu	Pro	Thr	Pro	Pro	His	Val	Thr	Leu	Gly	Ile	Gln	Cys	Arg	Thr	Val	
			100					105					110			
aag	gac	aaa	tca	cta	cac	ctg	agt	tct	gct	atc	ttg	gtt	ctt	tct	gtg	384
Lys	Asp	Lys	Ser	Leu	His	Leu	Ser	Ser	Ala	Ile	Leu	Val	Leu	Ser	Val	
		115					120					125				
acc	aaa	cag	tct	gta	cgc	ccc	ctg	cag	agg	aac	cag	cat	ctg	gct	gac	432
Thr	Lys	Gln	Ser	Val	Arg	Pro	Leu	Gln	Arg	Asn	Gln	His	Leu	Ala	Asp	
	130					135					140					
atc	tcc	aca	ggc	gca	gca	acc	acc	tgc	tgg	cca	gaa	gag	gta	aca	tta	480
Ile	Ser	Thr	Gly	Ala	Ala	Thr	Thr	Cys	Trp	Pro	Glu	Glu	Val	Thr	Leu	
145				150					155						160	
gta	gca	tat	tca	gtt	cac	acc	gaa	cgt	cat	tat	gaa	aat	cag	cag	aac	528
Val	Ala	Tyr	Ser	Val	His	Thr	Glu	Arg	His	Tyr	Glu	Asn	Gln	Gln	Asn	
			165					170						175		
gga	aca	cca	gaa	agg	tcc	agt	gac	agg	ccc	cga	ggc	cac	agg	gca	ggg	576
Gly	Thr	Pro	Glu	Arg	Ser	Ser	Asp	Arg	Pro	Arg	Gly	His	Arg	Ala	Gly	
		180					185					190				

624

657

<210> 206
<211> 218
<212> PRT
<213> Homo sapiens

<400> 206															
Met 1	Arg	Asp	Lys	Ala 5	Ala	Pro	Ala	Trp	Thr 10	Val	Leu	Ala	Leu 15	Met	Gln
Gly	Val	Gln	Ala 20	Lys	Lys	Glu	Arg	Pro 25	Ser	Trp	Leu	Arg	Asp 30	Ala	Val
Leu	Cys	Ser	Thr	Thr	Pro	Val	Pro	Arg	Ala	Phe	Pro	Met	Ala	Lys	His
Gln	His	Leu	Pro	Leu	Phe	Lys	Ser	Leu	Ser	Val	Ala	Gln	Gln	Lys	Thr
Arg 65	His	Asp	Thr	Tyr	Leu	Arg	Phe	Asn	Ile	Leu	Ile	Leu	Arg	Leu	Tyr
Asn	Thr	Gly	Tyr	Tyr	Trp	Gln	His	His	Glu	Thr	Lys	Lys	Gln	Lys	Leu
Leu	Pro	Thr	Pro	Pro	His	Val	Thr	Leu	Gly	Ile	Gln	Cys	Arg	Thr	Val
Lys	Asp	Lys	Ser	Leu	His	Leu	Ser	Ser	Ala	Ile	Leu	Val	Leu	Ser	Val
Thr	Lys	Gln	Ser	Val	Arg	Pro	Leu	Gln	Arg	Asn	Gln	His	Leu	Ala	Asp
Ile 145	Ser	Thr	Gly	Ala	Ala	Thr	Thr	Cys	Trp	Pro	Glu	Glu	Val	Thr	Leu
Val	Ala	Tyr	Ser	Val	His	Thr	Glu	Arg	His	Tyr	Glu	Asn	Gln	Gln	Asn
Gly	Thr	Pro	Glu	Arg	Ser	Ser	Asp	Arg	Pro	Arg	Gly	His	Arg	Ala	Gly
Lys	Leu	Ala	Asn	Glu	Leu	Ile	Ser	Ala	Asp	Val	His	Val	Cys	Thr	Phe
Tyr	Pro	Thr	Pro	Lys	Pro	Cys	Ala	Gly	Phe						

<210> 207
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(354)

<400> 207

atg agc cca ggc tat ttg ctg ctg ctg ctg ctg ttg gag tca cct gtt	48
Met Ser Pro Gly Tyr Leu Leu Leu Leu Leu Leu Leu Glu Ser Pro Val	
1 5 10 15	
gct gga agg aac tgt gcc act gta cta cac cag aac agc tgc cat ctc	96
Ala Gly Arg Asn Cys Ala Thr Val Leu His Gln Asn Ser Cys His Leu	
20 25 30	
cat gac aac aag cac gcg ctg gtg ctg cct gcc tgg agg gga gaa gag	144
His Asp Asn Lys His Ala Leu Val Leu Pro Ala Trp Arg Gly Glu Glu	
35 40 45	
cac aga gaa ggc att agc tac tgc cct ccc aga cgc agg aca agc gac	192
His Arg Glu Gly Ile Ser Tyr Cys Pro Pro Arg Arg Arg Thr Ser Asp	
50 55 60	
aga att tcc aac agc atc ggc tac tac ggc aac acc ttt tta ctc ttg	240
Arg Ile Ser Asn Ser Ile Gly Tyr Tyr Gly Asn Thr Phe Leu Leu Leu	
65 70 75 80	
tgc acc aaa ctg gcc gac atc tcg gaa caa gga ggg gac tgg cct tcc	288
Cys Thr Lys Leu Ala Asp Ile Ser Glu Gln Gly Gly Asp Trp Pro Ser	
85 90 95	
cag atc cac aat gcc gcg gaa gca gag cca gcc gcc tct cca ctc tcc	336
Gln Ile His Asn Ala Ala Glu Ala Glu Pro Ala Ala Ser Pro Leu Ser	
100 105 110	
gcc aac cgc gac aag taa	354
Ala Asn Arg Asp Lys *	
115	

<210> 208
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 208
 Met Ser Pro Gly Tyr Leu Leu Leu Leu Leu Leu Glu Ser Pro Val
 1 5 10 15
 Ala Gly Arg Asn Cys Ala Thr Val Leu His Gln Asn Ser Cys His Leu
 20 25 30
 His Asp Asn Lys His Ala Leu Val Leu Pro Ala Trp Arg Gly Glu Glu
 35 40 45
 His Arg Glu Gly Ile Ser Tyr Cys Pro Pro Arg Arg Arg Thr Ser Asp
 50 55 60
 Arg Ile Ser Asn Ser Ile Gly Tyr Tyr Gly Asn Thr Phe Leu Leu Leu
 65 70 75 80
 Cys Thr Lys Leu Ala Asp Ile Ser Glu Gln Gly Gly Asp Trp Pro Ser
 85 90 95
 Gln Ile His Asn Ala Ala Glu Ala Glu Pro Ala Ala Ser Pro Leu Ser
 100 105 110
 Ala Asn Arg Asp Lys
 115

<210> 209
 <211> 693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(693)

<400> 209
 atg ggc tcc ccg gcc acc gcc gcc acc ggg ctc ctc ctc ctg ctg ctg 48
 Met Gly Ser Pro Ala Thr Ala Ala Thr Gly Leu Leu Leu Leu Leu Leu
 1 5 10 15
 ctg ctg ctg ctg ctg ccg ccg cgg ctc ggc cgg gag aga aaa ggg ctg 96
 Leu Leu Leu Leu Leu Pro Pro Arg Leu Gly Arg Glu Arg Lys Gly Leu
 20 25 30
 agg gaa acg tgg tcc ctt ata tta ctt tca gcc gtg ggt tgt cct gag 144

Arg	Glu	Thr	Trp	Ser	Leu	Ile	Leu	Leu	Ser	Ala	Val	Gly	Cys	Pro	Glu		
		35					40					45					
ctg	ata	gca	cgc	gat	gat	cga	tgg	ttg	gac	ctt	aac	tgc	cgt	act	cat	192	
Leu	Ile	Ala	Arg	Asp	Asp	Arg	Trp	Leu	Asp	Leu	Asn	Cys	Arg	Thr	His		
	50					55					60						
agt	gga	gac	act	atc	gca	tac	ccg	ttg	tcg	tgt	tcg	act	aat	ccc	gtt	240	
Ser	Gly	Asp	Thr	Ile	Ala	Tyr	Pro	Leu	Ser	Cys	Ser	Thr	Asn	Pro	Val		
	65				70					75					80		
cgc	ggc	ggc	ctt	gtc	aac	aac	gtg	ccc	ttt	ggc	cct	cca	tca	cga	atg	288	
Arg	Gly	Gly	Leu	Val	Asn	Asn	Val	Pro	Phe	Gly	Pro	Pro	Ser	Arg	Met		
				85					90					95			
tgc	agt	cat	tcg	atg	gct	gag	ggc	aag	atc	aca	cac	ttt	gtc	gtt	tct	336	
Cys	Ser	His	Ser	Met	Ala	Glu	Gly	Lys	Ile	Thr	His	Phe	Val	Val	Ser		
			100					105					110				
tct	act	ttg	gtg	gat	gtg	cct	cag	tgc	ccg	cat	ggc	gca	ctc	ctt	gca	384	
Ser	Thr	Leu	Val	Asp	Val	Pro	Gln	Cys	Pro	His	Gly	Ala	Leu	Leu	Ala		
			115				120					125					
ggc	ctc	cta	ctg	tgc	ctc	ccc	aag	gcc	act	gga	aga	acc	caa	act	gcc	432	
Gly	Leu	Leu	Leu	Cys	Leu	Pro	Lys	Ala	Thr	Gly	Arg	Thr	Gln	Thr	Ala		
	130					135					140						
atc	gga	ttt	cag	agt	gtc	ggc	gtc	tgc	gta	aga	tta	cgc	tcc	att	acc	480	
Ile	Gly	Phe	Gln	Ser	Val	Gly	Val	Cys	Val	Arg	Leu	Arg	Ser	Ile	Thr		
	145				150					155					160		
agt	agt	tgg	caa	gtt	cat	acg	ggc	cgc	cat	tgg	cac	gcc	atg	gag	ggc	528	
Ser	Ser	Trp	Gln	Val	His	Thr	Gly	Arg	His	Trp	His	Ala	Met	Glu	Gly		
				165				170						175			
tac	tac	aga	gat	aat	cct	ggc	tct	aaa	tca	tcg	gtg	acg	ggg	aca	gtc	576	
Tyr	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Lys	Ser	Ser	Val	Thr	Gly	Thr	Val		
			180					185					190				
tac	gac	atg	aca	tcc	tcc	aga	aaa	tcc	acc	gtg	ttg	gta	aag	gtg	ctc	624	
Tyr	Asp	Met	Thr	Ser	Ser	Arg	Lys	Ser	Thr	Val	Leu	Val	Lys	Val	Leu		
	195						200					205					

Ala Ile Glu Gly Arg Lys
225 230

<210> 211
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(307)

<400> 211

atg ctc ctg ctg ctg ctc ctt gaa aca ctg gct gtg ttt gca ctg agg 48
Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
1 5 10 15

cca tgc ctc agc cag cga ctg agt gtg aca agg att ctc agt cct gtt 96
Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
20 25 30

cct ggg aga tgt gag att cct ttg ctg gca aac ttc agc ttg aat att 144
Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
35 40 45

ccc cag gtt agc caa ttc cca gag ata ata caa caa ctt gct aca cta 192
Pro Gln Val Ser Gln Phe Pro Glu Ile Ile Gln Gln Leu Ala Thr Leu
50 55 60

gca tgc ttt tca ggt tca aat cta cca att caa agc cct tac acc caa 240
Ala Cys Phe Ser Gly Ser Asn Leu Pro Ile Gln Ser Pro Tyr Thr Gln
65 70 75 80

cca cct act tta tct ggc tct tgc act ctg ggt cac tat cca ctt gcc 288
Pro Pro Thr Leu Ser Gly Ser Cys Thr Leu Gly His Tyr Pro Leu Ala
85 90 95

cta atc acc tca gga cca g 307
Leu Ile Thr Ser Gly Pro
100

<210> 212

<211> 102
 <212> PRT
 <213> Homo sapiens

<400> 212

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Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
 1          5          10          15
Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
          20          25          30
Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
          35          40          45
Pro Gln Val Ser Gln Phe Pro Glu Ile Ile Gln Gln Leu Ala Thr Leu
          50          55          60
Ala Cys Phe Ser Gly Ser Asn Leu Pro Ile Gln Ser Pro Tyr Thr Gln
65          70          75          80
Pro Pro Thr Leu Ser Gly Ser Cys Thr Leu Gly His Tyr Pro Leu Ala
          85          90          95
Leu Ile Thr Ser Gly Pro
          100

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<210> 213
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(615)

<400> 213

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atg tca cct cca agc acc tcc tgg ggt tgc ctg tcc tct ctc ctc ttc      48
Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1          5          10          15

ctg ctg agc ccc tgg gtc caa gga cct ccc acc ttc aaa aaa gta aaa      96
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
          20          25          30

aca gca cag ccc aga ccc agg ggt aaa att cat gtc atc act tct tcc      144
Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
          35          40          45

tgg gcc agc acc caa ata cct cct gag cca cag gaa cac gat gcc tct      192

```

Trp	Ala	Ser	Thr	Gln	Ile	Pro	Pro	Glu	Pro	Gln	Glu	His	Asp	Ala	Ser		
50						55					60						
gtg	gcc	ctg	aca	gcc	act	gcc	gat	tgt	cct	ggg	agg	ggc	ctt	cag	gga	240	
Val	Ala	Leu	Thr	Ala	Thr	Ala	Asp	Cys	Pro	Gly	Arg	Gly	Leu	Gln	Gly		
65					70				75					80			
acc	gca	cag	gaa	gga	ggg	tgc	agc	tca	gcc	cgt	ttt	caa	atc	cag	cag	288	
Thr	Ala	Gln	Glu	Gly	Gly	Cys	Ser	Ser	Ala	Arg	Phe	Gln	Ile	Gln	Gln		
				85				90						95			
gat	gtt	cat	gac	ctc	cct	gca	gac	act	aat	gga	cag	aac	gtc	aca	gca	336	
Asp	Val	His	Asp	Leu	Pro	Ala	Asp	Thr	Asn	Gly	Gln	Asn	Val	Thr	Ala		
			100					105					110				
gtc	tgc	ttc	cct	cac	ctg	tac	ggg	ggt	tac	ccc	aga	tca	ccc	cca	gtc	384	
Val	Cys	Phe	Pro	His	Leu	Tyr	Gly	Gly	Tyr	Pro	Arg	Ser	Pro	Pro	Val		
		115					120					125					
acc	gac	tgc	atg	caa	atc	tct	gtc	tca	gag	ttt	ggt	ccc	agc	aca	ttc	432	
Thr	Asp	Cys	Met	Gln	Ile	Ser	Val	Ser	Glu	Phe	Gly	Pro	Ser	Thr	Phe		
	130					135					140						
aac	cta	ggg	cat	gta	gga	cca	ccc	tcg	ttt	cac	gat	aaa	caa	cca	aaa	480	
Asn	Leu	Gly	His	Val	Gly	Pro	Pro	Ser	Phe	His	Asp	Lys	Gln	Pro	Lys		
145					150				155					160			
cag	ggc	agt	tac	gtg	atg	tgc	gta	aga	tgg	cac	gac	tca	cac	gtg	ccg	528	
Gln	Gly	Ser	Tyr	Val	Met	Cys	Val	Arg	Trp	His	Asp	Ser	His	Val	Pro		
				165				170						175			
cag	ctg	gaa	ctt	aaa	ctc	cat	ccg	gac	tcc	aag	gcc	acc	ctg	ttg	tct	576	
Gln	Leu	Glu	Leu	Lys	Leu	His	Pro	Asp	Ser	Lys	Ala	Thr	Leu	Leu	Ser		
			180					185					190				
ctc	cac	aat	caa	tgc	tca	gag	cac	agc	ctg	caa	ctg	taa				615	
Leu	His	Asn	Gln	Cys	Ser	Glu	His	Ser	Leu	Gln	Leu	*					
		195				200											

<210> 214

<211> 204

<212> PRT

<213> Homo sapiens

<400> 214

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Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1          5          10          15
Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
          20          25          30
Thr Ala Gln Pro Arg Pro Arg Gly Lys Ile His Val Ile Thr Ser Ser
          35          40          45
Trp Ala Ser Thr Gln Ile Pro Pro Glu Pro Gln Glu His Asp Ala Ser
          50          55          60
Val Ala Leu Thr Ala Thr Ala Asp Cys Pro Gly Arg Gly Leu Gln Gly
65          70          75          80
Thr Ala Gln Glu Gly Gly Cys Ser Ser Ala Arg Phe Gln Ile Gln Gln
          85          90          95
Asp Val His Asp Leu Pro Ala Asp Thr Asn Gly Gln Asn Val Thr Ala
          100          105          110
Val Cys Phe Pro His Leu Tyr Gly Gly Tyr Pro Arg Ser Pro Pro Val
          115          120          125
Thr Asp Cys Met Gln Ile Ser Val Ser Glu Phe Gly Pro Ser Thr Phe
          130          135          140
Asn Leu Gly His Val Gly Pro Pro Ser Phe His Asp Lys Gln Pro Lys
145          150          155          160
Gln Gly Ser Tyr Val Met Cys Val Arg Trp His Asp Ser His Val Pro
          165          170          175
Gln Leu Glu Leu Lys Leu His Pro Asp Ser Lys Ala Thr Leu Leu Ser
          180          185          190
Leu His Asn Gln Cys Ser Glu His Ser Leu Gln Leu
          195          200

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<210> 215

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(483)

<400> 215

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atg cct gat gtc tgg ggt cca gct gct gct gcc agt gct gcc tct tct
Met Pro Asp Val Trp Gly Pro Ala Ala Ala Ala Ser Ala Ala Ser Ser
 1          5          10          15

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gct gcc aac ccc act ctt ttc atc ctc ctg ctg ctt cca cca aca ttt	96
Ala Ala Asn Pro Thr Leu Phe Ile Leu Leu Leu Leu Pro Pro Thr Phe	
20 25 30	
ctg ctg cca tcg cca aaa tta cag atg ctg cca gca ctg cag ctt tgc	144
Leu Leu Pro Ser Pro Lys Leu Gln Met Leu Pro Ala Leu Gln Leu Cys	
35 40 45	
ttc ccc cct gct gtc ttg ttg ctg cat tgc cat ggc atc agg caa ggg	192
Phe Pro Pro Ala Val Leu Leu Leu His Cys His Gly Ile Arg Gln Gly	
50 55 60	
ttc agg ggc cta ggc aaa tgg act gtg gca ctt gta tgt ctc cct cct	240
Phe Arg Gly Leu Gly Lys Trp Thr Val Ala Leu Val Cys Leu Pro Pro	
65 70 75 80	
gga aaa tgc agg cta tcc aat aaa ggg gag aga gga aca ggg cag agc	288
Gly Lys Cys Arg Leu Ser Asn Lys Gly Glu Arg Gly Thr Gly Gln Ser	
85 90 95	
act ata aaa ggc aaa cac cgt ggt gaa att tgc agc acc atc cgg ctg	336
Thr Ile Lys Gly Lys His Arg Gly Glu Ile Cys Ser Thr Ile Arg Leu	
100 105 110	
cca aat tta gca tcc agg tca ctg gtg cca cgg aaa gcg ttg cca ctg	384
Pro Asn Leu Ala Ser Arg Ser Leu Val Pro Arg Lys Ala Leu Pro Leu	
115 120 125	
atg ctt gtg ccg gga aag gca cct ctc ctc tgc ttc agt gtc cat gct	432
Met Leu Val Pro Gly Lys Ala Pro Leu Leu Cys Phe Ser Val His Ala	
130 135 140	
aag gga aac cta atg cct cac act gac aaa aat gca ccc agt gga tct	480
Lys Gly Asn Leu Met Pro His Thr Asp Lys Asn Ala Pro Ser Gly Ser	
145 150 155 160	
taa	483
*	

217

<211> 160
 <212> PRT
 <213> Homo sapiens

<400> 216

Met	Pro	Asp	Val	Trp	Gly	Pro	Ala	Ala	Ala	Ala	Ser	Ala	Ala	Ser	Ser
1				5				10						15	
Ala	Ala	Asn	Pro	Thr	Leu	Phe	Ile	Leu	Leu	Leu	Leu	Pro	Pro	Thr	Phe
			20					25					30		
Leu	Leu	Pro	Ser	Pro	Lys	Leu	Gln	Met	Leu	Pro	Ala	Leu	Gln	Leu	Cys
		35					40					45			
Phe	Pro	Pro	Ala	Val	Leu	Leu	Leu	His	Cys	His	Gly	Ile	Arg	Gln	Gly
		50				55					60				
Phe	Arg	Gly	Leu	Gly	Lys	Trp	Thr	Val	Ala	Leu	Val	Cys	Leu	Pro	Pro
65					70					75					80
Gly	Lys	Cys	Arg	Leu	Ser	Asn	Lys	Gly	Glu	Arg	Gly	Thr	Gly	Gln	Ser
			85					90					95		
Thr	Ile	Lys	Gly	Lys	His	Arg	Gly	Glu	Ile	Cys	Ser	Thr	Ile	Arg	Leu
			100					105					110		
Pro	Asn	Leu	Ala	Ser	Arg	Ser	Leu	Val	Pro	Arg	Lys	Ala	Leu	Pro	Leu
		115					120					125			
Met	Leu	Val	Pro	Gly	Lys	Ala	Pro	Leu	Leu	Cys	Phe	Ser	Val	His	Ala
	130					135					140				
Lys	Gly	Asn	Leu	Met	Pro	His	Thr	Asp	Lys	Asn	Ala	Pro	Ser	Gly	Ser
145					150					155					160

<210> 217
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(240)

<400> 217

atg	acc	aac	aga	ttc	ttg	ctc	ctg	tta	tct	tct	ttc	cag	cag	gtc	tat	48
Met	Thr	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ser	Ser	Phe	Gln	Gln	Val	Tyr	
1				5					10					15		
ggg	gac	cgt	aaa	act	gtt	aaa	gac	ttt	tgt	tca	ggc	tcc	ctc	aac	agt	96
Gly	Asp	Arg	Lys	Thr	Val	Lys	Asp	Phe	Cys	Ser	Gly	Ser	Leu	Asn	Ser	
			20					25					30			

1	5	10	15	
caa gcc ctc agg gct ctg cag gac aat cct cgg cgt ctg ctg ctg ctg				96
Gln Ala Leu Arg Ala Leu Gln Asp Asn Pro Arg Arg Leu Leu Leu Leu				
	20	25	30	
ctg ctg ctg ctg gaa cct tct cag ggt gtc ctc tgc tgg cag gca ggc				144
Leu Leu Leu Leu Glu Pro Ser Gln Gly Val Leu Cys Trp Gln Ala Gly				
	35	40	45	
ttc gca cac agc ctc tgc cag ggc tgt gca cag cag gca gca cca ggc				192
Phe Ala His Ser Leu Cys Gln Gly Cys Ala Gln Gln Ala Ala Pro Gly				
	50	55	60	
cac agc att gac tgg cta ttt gtg caa cgc tgg ttg aag acg cca gtg				240
His Ser Ile Asp Trp Leu Phe Val Gln Arg Trp Leu Lys Thr Pro Val				
	65	70	75	80
acc tgg aaa agg gcc caa gcc agg ccg cgg ccg cgg ctc ctc gac tcc				288
Thr Trp Lys Arg Ala Gln Ala Arg Pro Arg Pro Arg Leu Leu Asp Ser				
	85	90	95	
tcc ggt cac ctg gcc cca gcc tgg gac cgc tcc cgc ctc cag ccg ctg				336
Ser Gly His Leu Ala Pro Ala Trp Asp Arg Ser Arg Leu Gln Pro Leu				
	100	105	110	
gaa agc atc tcc agg ctg gtg gcg cgg act ttc atg gaa aca tca cct				384
Glu Ser Ile Ser Arg Leu Val Ala Arg Thr Phe Met Glu Thr Ser Pro				
	115	120	125	
ctc ttc aaa gga tcc ttg gat ccc cca aaa gag aac acc agc tct ggg				432
Leu Phe Lys Gly Ser Leu Asp Pro Pro Lys Glu Asn Thr Ser Ser Gly				
	130	135	140	
atc gcc agg ccc tgg ctc agc tct cca ccc tgt aat gaa atg gcc agc				480
Ile Ala Arg Pro Trp Leu Ser Ser Pro Pro Cys Asn Glu Met Ala Ser				
	145	150	155	160
tat ctg gga cat tac tgt agc ctc ctc gcc atc aga act gtc act ccc				528
Tyr Leu Gly His Tyr Cys Ser Leu Leu Ala Ile Arg Thr Val Thr Pro				
	165	170	175	
gct gcc atc atc ctc tcc ttc agc acc atc tcc att ctc atc act cgc				576

Ala Ala Ile Ile Leu Ser Phe Ser Thr Ile Ser Ile Leu Ile Thr Arg
 180 185 190

atc acc acc acc tca cac aga acc atc tgc atc ctt ctg ctc acc cag 624
 Ile Thr Thr Thr Ser His Arg Thr Ile Cys Ile Leu Leu Leu Thr Gln
 195 200 205

tgg acc ctc ttc tcc ctg tac cca ggg agg aac cct atc agc att tgc 672
 Trp Thr Leu Phe Ser Leu Tyr Pro Gly Arg Asn Pro Ile Ser Ile Cys
 210 215 220

tgc ctt tga 681
 Cys Leu *
 225

<210> 220
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 220
 Met Asn Leu Gln His Gln Pro Leu Pro Val Ser His Ser Gln Gly Gly
 1 5 10 15
 Gln Ala Leu Arg Ala Leu Gln Asp Asn Pro Arg Arg Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Glu Pro Ser Gln Gly Val Leu Cys Trp Gln Ala Gly
 35 40 45
 Phe Ala His Ser Leu Cys Gln Gly Cys Ala Gln Gln Ala Ala Pro Gly
 50 55 60
 His Ser Ile Asp Trp Leu Phe Val Gln Arg Trp Leu Lys Thr Pro Val
 65 70 75 80
 Thr Trp Lys Arg Ala Gln Ala Arg Pro Arg Pro Arg Leu Leu Asp Ser
 85 90 95
 Ser Gly His Leu Ala Pro Ala Trp Asp Arg Ser Arg Leu Gln Pro Leu
 100 105 110
 Glu Ser Ile Ser Arg Leu Val Ala Arg Thr Phe Met Glu Thr Ser Pro
 115 120 125
 Leu Phe Lys Gly Ser Leu Asp Pro Pro Lys Glu Asn Thr Ser Ser Gly
 130 135 140
 Ile Ala Arg Pro Trp Leu Ser Ser Pro Pro Cys Asn Glu Met Ala Ser
 145 150 155 160
 Tyr Leu Gly His Tyr Cys Ser Leu Leu Ala Ile Arg Thr Val Thr Pro

165 170 175
 Ala Ala Ile Ile Leu Ser Phe Ser Thr Ile Ser Ile Leu Ile Thr Arg
 180 185 190
 Ile Thr Thr Thr Ser His Arg Thr Ile Cys Ile Leu Leu Leu Thr Gln
 195 200 205
 Trp Thr Leu Phe Ser Leu Tyr Pro Gly Arg Asn Pro Ile Ser Ile Cys
 210 215 220
 Cys Leu
 225

<210> 221
 <211> 441
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(441)

<400> 221
 atg aca agg ctt ttt tgg ctg tgt gtg tcc agc tgt tcc atg cca gga 48
 Met Thr Arg Leu Phe Trp Leu Cys Val Ser Ser Cys Ser Met Pro Gly
 1 5 10 15
 gga gga gga gtt aca tgc tgg aag ctt gca gat agc ctg ggg ctg ctg 96
 Gly Gly Gly Val Thr Cys Trp Lys Leu Ala Asp Ser Leu Gly Leu Leu
 20 25 30
 ctc gcc ttg ctg cgg ttg gtg gca gct acc gag act acc tcg cac cag 144
 Leu Ala Leu Leu Arg Leu Val Ala Ala Thr Glu Thr Thr Ser His Gln
 35 40 45
 agc ggc ctg gcc ggg cag gcc ccg cag cgc tcc tac tcc ctc ttc ccg 192
 Ser Gly Leu Ala Gly Gln Ala Pro Gln Arg Ser Tyr Ser Leu Phe Pro
 50 55 60
 gcc cct gga ctt gcg gct gct gcc aca act agc gca gat gtc act ata 240
 Ala Pro Gly Leu Ala Ala Ala Ala Thr Thr Ser Ala Asp Val Thr Ile
 65 70 75 80
 acc atc gct gct gtt gcc ctc aat gca ctg gcc cac cct aca aag ctc 288
 Thr Ile Ala Ala Val Ala Leu Asn Ala Leu Ala His Pro Thr Lys Leu
 85 90 95

145

<210> 223
 <211> 576
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(576)

<400> 223

atg	aag	gca	tcc	tgg	gtg	cac	ctg	gcg	ctc	tgc	ctg	gcc	cac	agc	gca	48
Met	Lys	Ala	Ser	Trp	Val	His	Leu	Ala	Leu	Cys	Leu	Ala	His	Ser	Ala	
1				5					10					15		

cgt	ggg	gca	gac	ctc	agg	ccg	cag	tca	cgg	ggc	tgc	tca	ggt	gct	gcg	96
Arg	Gly	Ala	Asp	Leu	Arg	Pro	Gln	Ser	Arg	Gly	Cys	Ser	Gly	Ala	Ala	
			20				25						30			

atg	gga	gaa	gag	cca	gga	agt	gag	tct	cca	ccc	agt	gcc	gct	cag	tca	144
Met	Gly	Glu	Glu	Pro	Gly	Ser	Glu	Ser	Pro	Pro	Ser	Ala	Ala	Gln	Ser	
		35					40					45				

cgg	gac	cca	gaa	ctc	act	gaa	ccg	ccc	acg	tta	atg	acg	cgc	agt	tcg	192
Arg	Asp	Pro	Glu	Leu	Thr	Glu	Pro	Pro	Thr	Leu	Met	Thr	Arg	Ser	Ser	
	50					55					60					

ccg	tgt	gcc	aat	gac	gcc	tca	atc	aag	ctg	cta	aac	gaa	ggc	cgg	agc	240
Pro	Cys	Ala	Asn	Asp	Ala	Ser	Ile	Lys	Leu	Leu	Asn	Glu	Gly	Arg	Ser	
65					70				75					80		

agc	cct	gcc	tgt	ggg	gct	gta	atg	ttt	tct	gca	gcc	ttg	atg	agc	cgc	288
Ser	Pro	Ala	Cys	Gly	Ala	Val	Met	Phe	Ser	Ala	Ala	Leu	Met	Ser	Arg	
				85					90					95		

cct	ggg	ctg	ttt	caa	agg	gaa	cgc	agc	agt	ctc	ctc	ttg	act	tcc	gca	336
Pro	Gly	Leu	Phe	Gln	Arg	Glu	Arg	Ser	Ser	Leu	Leu	Leu	Thr	Ser	Ala	
			100					105					110			

gtg	gcc	gta	ttc	ctg	ggc	cgt	gcg	gta	aac	agg	gag	tat	cta	ggc	tcg	384
Val	Ala	Val	Phe	Leu	Gly	Arg	Ala	Val	Asn	Arg	Glu	Tyr	Leu	Gly	Ser	
		115					120					125				

gat ggt tac aga cgg ctt tcc ccg tgg gcg gcg tcc cgt ggg ccc tat 432
 Asp Gly Tyr Arg Arg Leu Ser Pro Trp Ala Ala Ser Arg Gly Pro Tyr
 130 135 140

gca agc tgc gca ggc cgc cct ggg ctc tgc cgc gag tgc gtg ggc ggc 480
 Ala Ser Cys Ala Gly Arg Pro Gly Leu Cys Arg Glu Cys Val Gly Gly
 145 150 155 160

agg acg gtg cat ccc ggg cct cca ccg gtc aaa tgc tcc aca ctg acc 528
 Arg Thr Val His Pro Gly Pro Pro Pro Val Lys Cys Ser Thr Leu Thr
 165 170 175

acc gca gca ccc ccc cgc tct ccc ggg caa att cta aag ctt ccc tag 576
 Thr Ala Ala Pro Pro Arg Ser Pro Gly Gln Ile Leu Lys Leu Pro *
 180 185 190

<210> 224

<211> 191

<212> PRT

<213> Homo sapiens

<400> 224

Met Lys Ala Ser Trp Val His Leu Ala Leu Cys Leu Ala His Ser Ala
 1 5 10 15
 Arg Gly Ala Asp Leu Arg Pro Gln Ser Arg Gly Cys Ser Gly Ala Ala
 20 25 30
 Met Gly Glu Glu Pro Gly Ser Glu Ser Pro Pro Ser Ala Ala Gln Ser
 35 40 45
 Arg Asp Pro Glu Leu Thr Glu Pro Pro Thr Leu Met Thr Arg Ser Ser
 50 55 60
 Pro Cys Ala Asn Asp Ala Ser Ile Lys Leu Leu Asn Glu Gly Arg Ser
 65 70 75 80
 Ser Pro Ala Cys Gly Ala Val Met Phe Ser Ala Ala Leu Met Ser Arg
 85 90 95
 Pro Gly Leu Phe Gln Arg Glu Arg Ser Ser Leu Leu Leu Thr Ser Ala
 100 105 110
 Val Ala Val Phe Leu Gly Arg Ala Val Asn Arg Glu Tyr Leu Gly Ser
 115 120 125
 Asp Gly Tyr Arg Arg Leu Ser Pro Trp Ala Ala Ser Arg Gly Pro Tyr
 130 135 140
 Ala Ser Cys Ala Gly Arg Pro Gly Leu Cys Arg Glu Cys Val Gly Gly

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<210> 225
<211> 870
<212> DNA
<213> Homo sapiens
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<400> 225

ggg cca tca gga agc ttg ctt aga gca gct gag ctg gat tta aaa gtt 336
Gly Pro Ser Gly Ser Leu Leu Arg Ala Ala Glu Leu Asp Leu Lys Val
100 105 110

gtg aag gtt ttg tgt cag ccc cag gag ctg gat ggt tca ggt ccc atg	384
Val Lys Val Leu Cys Gln Pro Gln Glu Leu Asp Gly Ser Gly Pro Met	
115 120 125	
cag gga cgt gga ctt gtg cct gct cag cgc cgg cac tgt tct ttc agc	432
Gln Gly Arg Gly Leu Val Pro Ala Gln Arg Arg His Cys Ser Phe Ser	
130 135 140	
atc tac gag aag ctg atc cag ttc tgt gcc att gac gag ctt ggc acc	480
Ile Tyr Glu Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr	
145 150 155 160	
aac tac cca aag gat atg ttt gat ccc cat ggc tgg tct gag gac tcc	528
Asn Tyr Pro Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser	
165 170 175	
tac tat gag gca tta gcc aag gcc cag aaa att gag atg gac aaa ttg	576
Tyr Tyr Glu Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu	
180 185 190	
gaa aag gcc aaa aag gag cga aca aaa att gag ttt gtg acg ggc acc	624
Glu Lys Ala Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr	
195 200 205	
aaa aaa ggc acc acg acc aac gcc acg tcc acc acc act acc act gcc	672
Lys Lys Gly Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala	
210 215 220	
agc aca gct gtt gca gat gct cag aag aga aag agc aag tgg gat tcg	720
Ser Thr Ala Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser	
225 230 235 240	
gct atc cca gtg aca acg ata gcc cag ccc acc atc ctc acc acc aca	768
Ala Ile Pro Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr	
245 250 255	
gcc acc ctg cca gct gtt gtc acg gtc acc acc agc gcc agc ggc tcc	816
Ala Thr Leu Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser	
260 265 270	
aag acc acc gtc atc tct gct gtg ggc acc att gtg aag aag gcc aag	864
Lys Thr Thr Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys	

275

280

285

cag tga

Gln *

870

<210> 226

<211> 289

<212> PRT

<213> Homo sapiens

<400> 226

Met Asn Ser Ala Phe Leu Leu Leu Phe Ala Cys Ile Leu Thr Ala Leu
1 5 10 15

Leu Ser Ala Ser Cys Leu Phe Lys Gly Ile Asp Asn Thr Glu Ala Glu
20 25 30

Lys Arg Asp Pro Gln Glu Leu Val Ala Ser Phe Ser Glu Arg Val Arg
35 40 45

Asn Met Ser Pro Asp Glu Ile Lys Ile Pro Pro Glu Pro Pro Gly Arg
50 55 60

Cys Ser Asn His Leu Gln Asn His Val Thr Leu Arg Ala Arg Gln Pro
65 70 75 80

Asp Asn Lys Leu Gln Pro Leu Thr Gly Pro Ser Pro Trp Glu Ser Gly
85 90 95

Gly Pro Ser Gly Ser Leu Leu Arg Ala Ala Glu Leu Asp Leu Lys Val
100 105 110

Val Lys Val Leu Cys Gln Pro Gln Glu Leu Asp Gly Ser Gly Pro Met
115 120 125

Gln Gly Arg Gly Leu Val Pro Ala Gln Arg Arg His Cys Ser Phe Ser
130 135 140

Ile Tyr Glu Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr
145 150 155 160

Asn Tyr Pro Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser
165 170 175

Tyr Tyr Glu Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu
180 185 190

Glu Lys Ala Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr
195 200 205

Lys Lys Gly Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala
210 215 220

Ser Thr Ala Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser
225 230 235 240

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Ala Ile Pro Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr
 245 250 255
 Ala Thr Leu Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser
 260 265 270
 Lys Thr Thr Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys
 275 280 285
 Gln

<210> 227
 <211> 822
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(822)

<400> 227

atg cgc ctt ccc ggg gta ccc ctg gcg cgc cct gcg ctg ctg ctg ctg	48
Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu	
1 5 10 15	
ctg ccg ctg ctc gcg ccg ctg ctg gga acg ggt gcg ccg gcc gag ctg	96
Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu	
20 25 30	
cgg gtc cgc gtg cgg ctg ccg gac ggc cag gtg acc gag gag agc ctg	144
Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu	
35 40 45	
cag gcg gac agc gac gcg gac agc atc agc ctc gag ctg cgc aag ccc	192
Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro	
50 55 60	
gac ggc acc ctc gtc tcc ttc acc gcc gac ttc aag aag gat gtg aag	240
Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys	
65 70 75 80	
gtc ttc cgg gcc ctg atc ctg ggg gag ctg gag aag ggg cag agt cag	288
Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln	
85 90 95	

ttc cag gcc ctc tgc ttt gtc acc cag ctg cag cac aat gag atc atc 336
 Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile
 100 105 110

ccc agt gag gcc atg gcc aag ctc cgg cag aaa aat ccc cgg gca gtg 384
 Pro Ser Glu Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val
 115 120 125

cgg cag gcg gag gag gtt cgg ggt ctg gag cat ctg cac atg gat gtc 432
 Arg Gln Ala Glu Glu Val Arg Gly Leu Glu His Leu His Met Asp Val
 130 135 140

gct gtc aac ttc agc cag ggg gcc ctg ctg agc ccc cat ctc cac aac 480
 Ala Val Asn Phe Ser Gln Gly Ala Leu Leu Ser Pro His Leu His Asn
 145 150 155 160

gtg tgt gcc gag gcc gtg gat gcc atc tac acc cgc cag gag gat gtc 528
 Val Cys Ala Glu Ala Val Asp Ala Ile Tyr Thr Arg Gln Glu Asp Val
 165 170 175

cgg ttc tgg ctg gag caa ggt gtg gac agt tct gtg ttc gag gct ctg 576
 Arg Phe Trp Leu Glu Gln Gly Val Asp Ser Ser Val Phe Glu Ala Leu
 180 185 190

ccc aag gcc tca gag cag gcg gag ctg cct cgc tgc agg cag gtg ggg 624
 Pro Lys Ala Ser Glu Gln Ala Glu Leu Pro Arg Cys Arg Gln Val Gly
 195 200 205

gac cgc ggg aag ccc tgc gtc tgc cac tat ggc ctg agc ctg gcc tgg 672
 Asp Arg Gly Lys Pro Cys Val Cys His Tyr Gly Leu Ser Leu Ala Trp
 210 215 220

tac ccc tgc atg ctc aag tac tgc cac agc cgc gac cgg ccc acg ccc 720
 Tyr Pro Cys Met Leu Lys Tyr Cys His Ser Arg Asp Arg Pro Thr Pro
 225 230 235 240

tac aag tgt ggc atc cgc agc tgc cag aag agc tac agc ttt gac ttc 768
 Tyr Lys Cys Gly Ile Arg Ser Cys Gln Lys Ser Tyr Ser Phe Asp Phe
 245 250 255

tac gtg ccc cag agg cag ctg tgt ctc tgg gat gag gat ccc tac cca 816
 Tyr Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
 260 265 270

ggc tag
Gly *

822

<210> 228
<211> 273
<212> PRT
<213> Homo sapiens

<400> 228

Met	Arg	Leu	Pro	Gly	Val	Pro	Leu	Ala	Arg	Pro	Ala	Leu	Leu	Leu	Leu
1				5				10					15		
Leu	Pro	Leu	Leu	Ala	Pro	Leu	Leu	Gly	Thr	Gly	Ala	Pro	Ala	Glu	Leu
			20					25					30		
Arg	Val	Arg	Val	Arg	Leu	Pro	Asp	Gly	Gln	Val	Thr	Glu	Glu	Ser	Leu
		35					40					45			
Gln	Ala	Asp	Ser	Asp	Ala	Asp	Ser	Ile	Ser	Leu	Glu	Leu	Arg	Lys	Pro
		50				55					60				
Asp	Gly	Thr	Leu	Val	Ser	Phe	Thr	Ala	Asp	Phe	Lys	Lys	Asp	Val	Lys
65					70					75					80
Val	Phe	Arg	Ala	Leu	Ile	Leu	Gly	Glu	Leu	Glu	Lys	Gly	Gln	Ser	Gln
				85					90					95	
Phe	Gln	Ala	Leu	Cys	Phe	Val	Thr	Gln	Leu	Gln	His	Asn	Glu	Ile	Ile
			100					105					110		
Pro	Ser	Glu	Ala	Met	Ala	Lys	Leu	Arg	Gln	Lys	Asn	Pro	Arg	Ala	Val
		115					120					125			
Arg	Gln	Ala	Glu	Glu	Val	Arg	Gly	Leu	Glu	His	Leu	His	Met	Asp	Val
		130				135					140				
Ala	Val	Asn	Phe	Ser	Gln	Gly	Ala	Leu	Leu	Ser	Pro	His	Leu	His	Asn
145					150					155					160
Val	Cys	Ala	Glu	Ala	Val	Asp	Ala	Ile	Tyr	Thr	Arg	Gln	Glu	Asp	Val
				165					170					175	
Arg	Phe	Trp	Leu	Glu	Gln	Gly	Val	Asp	Ser	Ser	Val	Phe	Glu	Ala	Leu
		180						185					190		
Pro	Lys	Ala	Ser	Glu	Gln	Ala	Glu	Leu	Pro	Arg	Cys	Arg	Gln	Val	Gly
		195					200					205			
Asp	Arg	Gly	Lys	Pro	Cys	Val	Cys	His	Tyr	Gly	Leu	Ser	Leu	Ala	Trp
		210				215					220				
Tyr	Pro	Cys	Met	Leu	Lys	Tyr	Cys	His	Ser	Arg	Asp	Arg	Pro	Thr	Pro
225					230					235					240
Tyr	Lys	Cys	Gly	Ile	Arg	Ser	Cys	Gln	Lys	Ser	Tyr	Ser	Phe	Asp	Phe

"000000" 000000

Tyr Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
 245 250 255
 260 265 270

Gly

<210> 229
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(453)

<400> 229

atg gtg gta ttt acc ttg ctg ctg gtg ctg ctg ttg ttg ctg ctg cta 48
 Met Val Val Phe Thr Leu Leu Leu Val Leu Leu Leu Leu Leu Leu
 1 5 10 15

aca gct cta tgt aag gct ctg agt caa agc ctt ccc tat acc ctc tac 96
 Thr Ala Leu Cys Lys Ala Leu Ser Gln Ser Leu Pro Tyr Thr Leu Tyr
 20 25 30

agg cca cag tca tca cta tcc ttc ctc ctt atc act gat ata aaa aag 144
 Arg Pro Gln Ser Ser Leu Ser Phe Leu Leu Ile Thr Asp Ile Lys Lys
 35 40 45

att gat ata cag tat ttt ctc cca ttg aca ggt ggc aag tgc ctg cat 192
 Ile Asp Ile Gln Tyr Phe Leu Pro Leu Thr Gly Gly Lys Cys Leu His
 50 55 60

ctt cgc ttg aca gga cag agg gct ttc tgt atc ctg gag ttc ttg cct 240
 Leu Arg Leu Thr Gly Gln Arg Ala Phe Cys Ile Leu Glu Phe Leu Pro
 65 70 75 80

tgg tgt aat gga ata att gaa tca ctc gtg ggc ttg gag aat gag cgc 288
 Trp Cys Asn Gly Ile Ile Glu Ser Leu Val Gly Leu Glu Asn Glu Arg
 85 90 95

aag gtt ttg agt gga ggt agc tct cag cag atg ggg gaa gcc aga agg 336
 Lys Val Leu Ser Gly Gly Ser Ser Gln Gln Met Gly Glu Ala Arg Arg
 100 105 110

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(768)

<400> 231

atg	cgc	ccc	cga	gcc	cca	gcc	tgc	gcc	gcc	gcg	gcg	ctc	ggg	ctc	tgc	48
Met	Arg	Pro	Arg	Ala	Pro	Ala	Cys	Ala	Ala	Ala	Ala	Leu	Gly	Leu	Cys	
1				5				10					15			

agc	ctt	ctg	ctg	ctg	ctc	gcg	ccc	ggg	cac	gcg	tgc	ccc	gcg	ggc	tgc	96
Ser	Leu	Leu	Leu	Leu	Leu	Ala	Pro	Gly	His	Ala	Cys	Pro	Ala	Gly	Cys	
			20					25					30			

gcc	tgc	acc	gac	ccg	cac	acc	gtg	gac	tgc	cgc	gac	cgc	ggg	ctg	ccc	144
Ala	Cys	Thr	Asp	Pro	His	Thr	Val	Asp	Cys	Arg	Asp	Arg	Gly	Leu	Pro	
		35					40					45				

agc	gtg	cca	gac	cct	ttc	ccc	ctg	gac	gtg	cgc	aag	ctg	ctg	gtg	gcc	192
Ser	Val	Pro	Asp	Pro	Phe	Pro	Leu	Asp	Val	Arg	Lys	Leu	Leu	Val	Ala	
	50					55					60					

ggc	aac	cgc	atc	cag	cgg	atc	ccc	gag	gac	ttc	ttc	atc	ttc	tac	ggc	240
Gly	Asn	Arg	Ile	Gln	Arg	Ile	Pro	Glu	Asp	Phe	Phe	Ile	Phe	Tyr	Gly	
65					70					75					80	

gac	ctg	gtc	tac	ctg	gac	ttc	agg	aac	aac	tcg	ctg	cgc	tcg	ctg	gag	288
Asp	Leu	Val	Tyr	Leu	Asp	Phe	Arg	Asn	Asn	Ser	Leu	Arg	Ser	Leu	Glu	
				85					90					95		

gag	ggc	acg	ttc	agc	ggc	tcg	gcc	aag	ctc	gtg	ttc	ctc	gac	ctc	agc	336
Glu	Gly	Thr	Phe	Ser	Gly	Ser	Ala	Lys	Leu	Val	Phe	Leu	Asp	Leu	Ser	
			100					105					110			

tac	aac	aac	ttg	acc	cag	ctg	ggc	gcc	ggc	gcc	ttc	cgc	tcg	gcc	ggg	384
Tyr	Asn	Asn	Leu	Thr	Gln	Leu	Gly	Ala	Gly	Ala	Phe	Arg	Ser	Ala	Gly	
			115				120					125				

agg	ctg	gtg	aag	ctt	agc	ctg	gct	aac	aac	aac	ctg	gtg	ggc	gtg	cac	432
Arg	Leu	Val	Lys	Leu	Ser	Leu	Ala	Asn	Asn	Asn	Leu	Val	Gly	Val	His	
	130						135					140				

gag gac gcc ttc gag acc ctg gag tcg ctg cag gtg ctg gag ctc aac 480
 Glu Asp Ala Phe Glu Thr Leu Glu Ser Leu Gln Val Leu Glu Leu Asn
 145 150 155 160

gac aac aac ctg cgc agc ctc agc gtg gcc gcc ctg gcc gcg ctg ccc 528
 Asp Asn Asn Leu Arg Ser Leu Ser Val Ala Ala Leu Ala Ala Leu Pro
 165 170 175

gcg ctg cgc tcc ctg cgt ctg gac ggg aac ccc tgg ctg tgc gac tgt 576
 Ala Leu Arg Ser Leu Arg Leu Asp Gly Asn Pro Trp Leu Cys Asp Cys
 180 185 190

gac ttc gcc cac ctc ttc tcc tgg atc cag gag aac gca tcc aaa ctg 624
 Asp Phe Ala His Leu Phe Ser Trp Ile Gln Glu Asn Ala Ser Lys Leu
 195 200 205

ccc aaa gga ctg gcg ggt gtg gat tac tta tgc gtc cct ggt aag cgg 672
 Pro Lys Gly Leu Ala Gly Val Asp Tyr Leu Cys Val Pro Gly Lys Arg
 210 215 220

aat gca gcc tac tct atg gga aac ggc cgt att ctc agt acc gtg cac 720
 Asn Ala Ala Tyr Ser Met Gly Asn Gly Arg Ile Leu Ser Thr Val His
 225 230 235 240

ggg gag tca gcc agt tcc aag ggc tct cca gca gct tcc cga gcc taa 768
 Gly Glu Ser Ala Ser Ser Lys Gly Ser Pro Ala Ala Ser Arg Ala *
 245 250 255

<210> 232

<211> 255

<212> PRT

<213> Homo sapiens

<400> 232

Met Arg Pro Arg Ala Pro Ala Cys Ala Ala Ala Ala Leu Gly Leu Cys
 1 5 10 15
 Ser Leu Leu Leu Leu Leu Ala Pro Gly His Ala Cys Pro Ala Gly Cys
 20 25 30
 Ala Cys Thr Asp Pro His Thr Val Asp Cys Arg Asp Arg Gly Leu Pro
 35 40 45
 Ser Val Pro Asp Pro Phe Pro Leu Asp Val Arg Lys Leu Leu Val Ala

50 55 60
 Gly Asn Arg Ile Gln Arg Ile Pro Glu Asp Phe Phe Ile Phe Tyr Gly
 65 70 75 80
 Asp Leu Val Tyr Leu Asp Phe Arg Asn Asn Ser Leu Arg Ser Leu Glu
 85 90 95
 Glu Gly Thr Phe Ser Gly Ser Ala Lys Leu Val Phe Leu Asp Leu Ser
 100 105 110
 Tyr Asn Asn Leu Thr Gln Leu Gly Ala Gly Ala Phe Arg Ser Ala Gly
 115 120 125
 Arg Leu Val Lys Leu Ser Leu Ala Asn Asn Asn Leu Val Gly Val His
 130 135 140
 Glu Asp Ala Phe Glu Thr Leu Glu Ser Leu Gln Val Leu Glu Leu Asn
 145 150 155 160
 Asp Asn Asn Leu Arg Ser Leu Ser Val Ala Ala Leu Ala Ala Leu Pro
 165 170 175
 Ala Leu Arg Ser Leu Arg Leu Asp Gly Asn Pro Trp Leu Cys Asp Cys
 180 185 190
 Asp Phe Ala His Leu Phe Ser Trp Ile Gln Glu Asn Ala Ser Lys Leu
 195 200 205
 Pro Lys Gly Leu Ala Gly Val Asp Tyr Leu Cys Val Pro Gly Lys Arg
 210 215 220
 Asn Ala Ala Tyr Ser Met Gly Asn Gly Arg Ile Leu Ser Thr Val His
 225 230 235 240
 Gly Glu Ser Ala Ser Ser Lys Gly Ser Pro Ala Ala Ser Arg Ala
 245 250 255

<210> 233
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(615)

<400> 233

atg tca cct cca agc acc tcc tgg ggt tgc ctg tcc tct ctc ctc ttc 48
 Met Ser Pro Pro Ser Thr Ser Trp Gly Cys Leu Ser Ser Leu Leu Phe
 1 5 10 15

ctg ctg agc ccc tgg gtc caa gga cct ccc acc ttc aaa aaa gta aaa 96
 Leu Leu Ser Pro Trp Val Gln Gly Pro Pro Thr Phe Lys Lys Val Lys
 20 25 30

aca	gca	cag	ccc	aga	ccc	agg	ggt	aaa	att	cat	gtc	atc	act	tct	tcc	144
Thr	Ala	Gln	Pro	Arg	Pro	Arg	Gly	Lys	Ile	His	Val	Ile	Thr	Ser	Ser	
		35					40					45				
tgg	gcc	agc	acc	caa	ata	cct	cct	gag	cca	cag	gaa	cac	gat	gcc	tct	192
Trp	Ala	Ser	Thr	Gln	Ile	Pro	Pro	Glu	Pro	Gln	Glu	His	Asp	Ala	Ser	
	50					55					60					
gtg	gcc	ctg	aca	gcc	act	gcc	gat	tgt	cct	ggg	agg	ggc	ctt	cag	gga	240
Val	Ala	Leu	Thr	Ala	Thr	Ala	Asp	Cys	Pro	Gly	Arg	Gly	Leu	Gln	Gly	
65					70					75					80	
acc	gca	cag	gaa	gga	ggg	tgc	agc	tca	gcc	cgt	ttt	caa	atc	cag	cag	288
Thr	Ala	Gln	Glu	Gly	Gly	Cys	Ser	Ser	Ala	Arg	Phe	Gln	Ile	Gln	Gln	
				85					90					95		
gat	gtt	cat	gac	ctc	cct	gca	gac	act	aat	gga	cag	aac	gtc	aca	gca	336
Asp	Val	His	Asp	Leu	Pro	Ala	Asp	Thr	Asn	Gly	Gln	Asn	Val	Thr	Ala	
			100					105					110			
gtc	tgc	ttc	cct	cac	ctg	tac	ggg	ggt	tac	ccc	aga	tca	ccc	cca	gtc	384
Val	Cys	Phe	Pro	His	Leu	Tyr	Gly	Gly	Tyr	Pro	Arg	Ser	Pro	Pro	Val	
		115					120					125				
acc	gac	tgc	atg	caa	atc	tct	gtc	tca	gag	ttt	ggt	ccc	agc	aca	ttc	432
Thr	Asp	Cys	Met	Gln	Ile	Ser	Val	Ser	Glu	Phe	Gly	Pro	Ser	Thr	Phe	
	130					135					140					
aac	cta	ggg	cat	gta	gga	cca	ccc	tcg	ttt	cac	gat	aaa	caa	cca	aaa	480
Asn	Leu	Gly	His	Val	Gly	Pro	Pro	Ser	Phe	His	Asp	Lys	Gln	Pro	Lys	
145					150					155					160	
cag	ggc	agt	tac	gtg	atg	tgc	gta	aga	tgg	cac	gac	tca	cac	gtg	ccg	528
Gln	Gly	Ser	Tyr	Val	Met	Cys	Val	Arg	Trp	His	Asp	Ser	His	Val	Pro	
				165				170						175		
cag	ctg	gaa	ctt	aaa	ctc	cat	ccg	gac	tcc	aag	gcc	acc	ctg	ttg	tct	576
Gln	Leu	Glu	Leu	Lys	Leu	His	Pro	Asp	Ser	Lys	Ala	Thr	Leu	Leu	Ser	
			180					185					190			
ctc	cac	aat	caa	tgc	tca	gag	cac	agc	ctg	caa	ctg	taa				615
Leu	His	Asn	Gln	Cys	Ser	Glu	His	Ser	Leu	Gln	Leu	*				

195

200

<210> 234

<211> 204

<212> PRT

<213> Homo sapiens

<400> 234

Met	Ser	Pro	Pro	Ser	Thr	Ser	Trp	Gly	Cys	Leu	Ser	Ser	Leu	Leu	Phe
1				5					10					15	
Leu	Leu	Ser	Pro	Trp	Val	Gln	Gly	Pro	Pro	Thr	Phe	Lys	Lys	Val	Lys
			20				25						30		
Thr	Ala	Gln	Pro	Arg	Pro	Arg	Gly	Lys	Ile	His	Val	Ile	Thr	Ser	Ser
		35					40					45			
Trp	Ala	Ser	Thr	Gln	Ile	Pro	Glu	Pro	Gln	Glu	His	Asp	Ala	Ser	
	50				55				60						
Val	Ala	Leu	Thr	Ala	Thr	Ala	Asp	Cys	Pro	Gly	Arg	Gly	Leu	Gln	Gly
65					70					75				80	
Thr	Ala	Gln	Glu	Gly	Gly	Cys	Ser	Ser	Ala	Arg	Phe	Gln	Ile	Gln	Gln
			85						90					95	
Asp	Val	His	Asp	Leu	Pro	Ala	Asp	Thr	Asn	Gly	Gln	Asn	Val	Thr	Ala
			100					105					110		
Val	Cys	Phe	Pro	His	Leu	Tyr	Gly	Gly	Tyr	Pro	Arg	Ser	Pro	Pro	Val
		115					120					125			
Thr	Asp	Cys	Met	Gln	Ile	Ser	Val	Ser	Glu	Phe	Gly	Pro	Ser	Thr	Phe
	130					135					140				
Asn	Leu	Gly	His	Val	Gly	Pro	Pro	Ser	Phe	His	Asp	Lys	Gln	Pro	Lys
145					150					155				160	
Gln	Gly	Ser	Tyr	Val	Met	Cys	Val	Arg	Trp	His	Asp	Ser	His	Val	Pro
			165						170					175	
Gln	Leu	Glu	Leu	Lys	Leu	His	Pro	Asp	Ser	Lys	Ala	Thr	Leu	Leu	Ser
		180					185						190		
Leu	His	Asn	Gln	Cys	Ser	Glu	His	Ser	Leu	Gln	Leu				
		195					200								

<210> 235

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

T00230.22E6660

Gly Thr Pro Leu Leu Phe
195

<210> 237
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(327)

<400> 237

atg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	ctg	cta	ctg	ctg	cta	tta	cca	48
Met	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	
1				5					10					15		

cgt	gag	ccc	acc	ttt	gtg	cta	atc	aag	act	cgc	atc	act	gcc	tta	aaa	96
Arg	Glu	Pro	Thr	Phe	Val	Leu	Ile	Lys	Thr	Arg	Ile	Thr	Ala	Leu	Lys	
			20					25					30			

agt	ggg	cat	cct	aaa	acg	tcc	aag	gaa	aac	atc	agg	gga	cat	gag	atg	144
Ser	Gly	His	Pro	Lys	Thr	Ser	Lys	Glu	Asn	Ile	Arg	Gly	His	Glu	Met	
		35					40					45				

tca	gat	ggc	cct	cac	aac	caa	gca	ctc	tgt	ctt	gaa	gca	cta	gct	aag	192
Ser	Asp	Gly	Pro	His	Asn	Gln	Ala	Leu	Cys	Leu	Glu	Ala	Leu	Ala	Lys	
	50					55					60					

ctg	cga	atc	aag	ctg	ctt	att	tgg	tta	gga	gaa	cct	gtg	aaa	gac	cat	240
Leu	Arg	Ile	Lys	Leu	Leu	Ile	Trp	Leu	Gly	Glu	Pro	Val	Lys	Asp	His	
	65				70				75					80		

agc	ttg	cat	gcc	ctg	cgg	ttc	gac	tct	aga	aga	tcc	ccc	cca	gca	ggc	288
Ser	Leu	His	Ala	Leu	Arg	Phe	Asp	Ser	Arg	Arg	Ser	Pro	Pro	Ala	Gly	
				85				90						95		

cag	att	gta	gta	gtt	ccc	aac	ttt	ggc	tgc	aca	ttg	taa				327
Gln	Ile	Val	Val	Val	Pro	Asn	Phe	Gly	Cys	Thr	Leu	*				
			100					105								

<210> 238

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 238

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Met Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro
 1          5          10          15
Arg Glu Pro Thr Phe Val Leu Ile Lys Thr Arg Ile Thr Ala Leu Lys
          20          25          30
Ser Gly His Pro Lys Thr Ser Lys Glu Asn Ile Arg Gly His Glu Met
          35          40          45
Ser Asp Gly Pro His Asn Gln Ala Leu Cys Leu Glu Ala Leu Ala Lys
          50          55          60
Leu Arg Ile Lys Leu Leu Ile Trp Leu Gly Glu Pro Val Lys Asp His
65          70          75          80
Ser Leu His Ala Leu Arg Phe Asp Ser Arg Arg Ser Pro Pro Ala Gly
          85          90          95
Gln Ile Val Val Val Pro Asn Phe Gly Cys Thr Leu
          100          105

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<210> 239
 <211> 456
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(456)

<400> 239

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atg cct gct tca gac acc agc ccc ctt ctt cgc ctc atc gca ctg agt      48
Met Pro Ala Ser Asp Thr Ser Pro Leu Leu Arg Leu Ile Ala Leu Ser
 1          5          10          15

agt aac atc att gca att gtt ttt cta ata gac tgc tgt gtc tgc cca      96
Ser Asn Ile Ile Ala Ile Val Phe Leu Ile Asp Cys Cys Val Cys Pro
          20          25          30

cta gat ttc aag ctc tct aaa gag gcc cac gat agt gtc act caa atc      144
Leu Asp Phe Lys Leu Ser Lys Glu Ala His Asp Ser Val Thr Gln Ile
          35          40          45

ctc tcc aga cag ccc ttt gga aac ata ttc cat gtt cct ctt ctt agg      192

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<210> 241
<211> 579
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(579)

<400> 241																
atg	tat	agc	gcc	gat	ttt	ggc	ctg	ctt	gca	ctg	cta	ccg	ctg	ccg	agc	48
Met	Tyr	Ser	Ala	Asp	Phe	Gly	Leu	Leu	Ala	Leu	Leu	Pro	Leu	Pro	Ser	
1			5			10			15							
caa	ggc	gcg	ccg	atg	gcc	acg	acg	ccc	tta	ccg	ggc	gcc	cct	acc	cca	96
Gln	Gly	Ala	Pro	Met	Ala	Thr	Thr	Pro	Leu	Pro	Gly	Ala	Pro	Thr	Pro	
20			25			30										
tgg	gat	gtt	gcg	att	aca	acc	aac	tgg	acc	ggc	gct	tac	cgc	aaa	gaa	144
Trp	Asp	Val	Ala	Ile	Thr	Thr	Asn	Trp	Thr	Gly	Ala	Tyr	Arg	Lys	Glu	
35			40			45										
tat	gcc	ctg	cac	gcg	gct	tgt	acc	ggg	caa	caa	aaa	aca	aaa	ata	caa	192
Tyr	Ala	Leu	His	Ala	Ala	Cys	Thr	Gly	Gln	Gln	Lys	Thr	Lys	Ile	Gln	
50			55			60										
aaa	cgc	gtg	cgc	ata	gct	ata	cat	gtt	tgc	ctg	cgt	act	gca	cca	ctg	240
Lys	Arg	Val	Arg	Ile	Ala	Ile	His	Val	Cys	Leu	Arg	Thr	Ala	Pro	Leu	
65			70			75			80							
gat	aac	cta	tgt	aca	gga	ttt	gct	gta	aac	ccg	cct	tgg	cca	cct	gcc	288
Asp	Asn	Leu	Cys	Thr	Gly	Phe	Ala	Val	Asn	Pro	Pro	Trp	Pro	Pro	Ala	

Tyr Ala Leu His Ala Ala Cys Thr Gly Gln Gln Lys Thr Lys Ile Gln
 50 55 60
 Lys Arg Val Arg Ile Ala Ile His Val Cys Leu Arg Thr Ala Pro Leu
 65 70 75 80
 Asp Asn Leu Cys Thr Gly Phe Ala Val Asn Pro Pro Trp Pro Pro Ala
 85 90 95
 Glu Leu Thr Leu Ser Leu Gln Phe Ala Val Gly Leu His Leu Val Thr
 100 105 110
 Gly Gly Leu Pro Ile Val Gly Gly Ser Glu Gly Ser Leu Pro His Asp
 115 120 125
 His Thr Leu Thr Ala Ile Ala Ser Asn Pro Pro Thr Pro Ala Ala Glu
 130 135 140
 Leu Pro Leu Thr Arg His Gly Glu Arg Glu Arg Arg Arg Gln Leu Pro
 145 150 155 160
 Ala Val Ser Arg Leu Tyr Glu Asp Pro His Pro Pro Leu Gly Ala Leu
 165 170 175
 Asn Glu Arg Thr Gly Lys Arg Pro Asp Met Thr Val Val Gly Leu Thr
 180 185 190

<210> 243
 <211> 351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(351)

<400> 243

atg gct cgc aga cac tgc ttc tcc tac tgg tta ctg gta tgc tgg ttg 48
 Met Ala Arg Arg His Cys Phe Ser Tyr Trp Leu Leu Val Cys Trp Leu
 1 5 10 15

gtg gta act gtg gca gaa gga caa gaa gag gta ttt acg cct cct gga 96
 Val Val Thr Val Ala Glu Gly Gln Glu Glu Val Phe Thr Pro Pro Gly
 20 25 30

gat tca caa aat aat gcg gac gct acc gac tgc cag atc ttt aca ctc 144
 Asp Ser Gln Asn Asn Ala Asp Ala Thr Asp Cys Gln Ile Phe Thr Leu
 35 40 45

acc cct cca cct gcc ccg agg agt ccg ttc tgc tca gag aaa ggc cct 192
 Thr Pro Pro Pro Ala Pro Arg Ser Pro Phe Cys Ser Glu Lys Gly Pro

50 55 60

gtc ctg ctg ctg ggc ctt gag gaa gcc aag att ctc tgc aat gac tgt 240
 Val Leu Leu Leu Gly Leu Glu Glu Ala Lys Ile Leu Cys Asn Asp Cys
 65 70 75 80

aat gga cga tcc act gtt cag ttt cat ata tta ggc atg aaa tgt aag 288
 Asn Gly Arg Ser Thr Val Gln Phe His Ile Leu Gly Met Lys Cys Lys
 85 90 95

att tgt gaa tcc tat aat act gct caa gct gga gga cgt aga att tca 336
 Ile Cys Glu Ser Tyr Asn Thr Ala Gln Ala Gly Gly Arg Arg Ile Ser
 100 105 110

ctg gat cag caa tga 351
 Leu Asp Gln Gln *
 115

<210> 244
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 244

Met Ala Arg Arg His Cys Phe Ser Tyr Trp Leu Leu Val Cys Trp Leu
 1 5 10 15
 Val Val Thr Val Ala Glu Gly Gln Glu Glu Val Phe Thr Pro Pro Gly
 20 25 30
 Asp Ser Gln Asn Asn Ala Asp Ala Thr Asp Cys Gln Ile Phe Thr Leu
 35 40 45
 Thr Pro Pro Pro Ala Pro Arg Ser Pro Phe Cys Ser Glu Lys Gly Pro
 50 55 60
 Val Leu Leu Leu Gly Leu Glu Glu Ala Lys Ile Leu Cys Asn Asp Cys
 65 70 75 80
 Asn Gly Arg Ser Thr Val Gln Phe His Ile Leu Gly Met Lys Cys Lys
 85 90 95
 Ile Cys Glu Ser Tyr Asn Thr Ala Gln Ala Gly Gly Arg Arg Ile Ser
 100 105 110
 Leu Asp Gln Gln
 115

<210> 245

<211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(327)

<400> 245

atg ctc ctg ctg ctg ctc ctt gaa aca ctg gct gtg ttt gca ctg agg 48
 Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
 1 5 10 15

cca tgc ctc agc cag cga ctg agt gtg aca agg att ctc agt cct gtt 96
 Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
 20 25 30

cct ggg aga tgt gag att cct ttg ctg gca aac ttc agc ttg aat att 144
 Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
 35 40 45

ccc cag gta caa tgg gat acc cgt ggc tac act cta tca cat ctc ttc 192
 Pro Gln Val Gln Trp Asp Thr Arg Gly Tyr Thr Leu Ser His Leu Phe
 50 55 60

att cat ctt ctc agc aac tct cca ttg aac act tac act gtt cta gac 240
 Ile His Leu Leu Ser Asn Ser Pro Leu Asn Thr Tyr Thr Val Leu Asp
 65 70 75 80

act caa gaa aga gca ctc ctt aag gca gac aaa gtt gcc tgc cct caa 288
 Thr Gln Glu Arg Ala Leu Leu Lys Ala Asp Lys Val Ala Cys Pro Gln
 85 90 95

gaa gct act att cta gtg aaa gaa gac aaa caa aaa taa 327
 Glu Ala Thr Ile Leu Val Lys Glu Asp Lys Gln Lys *
 100 105

<210> 246
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 246

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Met Leu Leu Leu Leu Leu Leu Glu Thr Leu Ala Val Phe Ala Leu Arg
 1           5           10           15
Pro Cys Leu Ser Gln Arg Leu Ser Val Thr Arg Ile Leu Ser Pro Val
          20           25           30
Pro Gly Arg Cys Glu Ile Pro Leu Leu Ala Asn Phe Ser Leu Asn Ile
          35           40           45
Pro Gln Val Gln Trp Asp Thr Arg Gly Tyr Thr Leu Ser His Leu Phe
          50           55           60
Ile His Leu Leu Ser Asn Ser Pro Leu Asn Thr Tyr Thr Val Leu Asp
65           70           75           80
Thr Gln Glu Arg Ala Leu Leu Lys Ala Asp Lys Val Ala Cys Pro Gln
          85           90           95
Glu Ala Thr Ile Leu Val Lys Glu Asp Lys Gln Lys
          100          105

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<210> 247

<211> 438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(438)

<400> 247

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atg agt ttg ctg ttg ctg ctg ctg ctg ctg ctg ctg ttt aaa tgg      48
Met Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Lys Trp
 1           5           10           15

aaa aga aga gta gta agt ggt cat ctt ctc agc gtc tgg tgc tgg tcc      96
Lys Arg Arg Val Val Ser Gly His Leu Leu Ser Val Trp Cys Trp Ser
          20           25           30

cgc cca cac act gtg gca gag cag acc cac ctg ttg tca ctg gga aat      144
Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu Ser Leu Gly Asn
          35           40           45

gag ggg ctg cag gta ctg ccc tta gac aat gga gag gct tct gga ctg      192
Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Glu Ala Ser Gly Leu
          50           55           60

tca ctc caa ctt gga atc aaa tgg acc act gag aaa ccc gtg gaa gac      240

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Ser Leu Gln Leu Gly Ile Lys Trp Thr Thr Glu Lys Pro Val Glu Asp
65 70 75 80

agc agg tct aag gaa atc aca aag att aga aat gca tcc atg tgc acc 288
Ser Arg Ser Lys Glu Ile Thr Lys Ile Arg Asn Ala Ser Met Cys Thr
85 90 95

caa ctc cct cct agt gtg ggt ggg ggc acc tgc aat agt ctc tgg tac 336
Gln Leu Pro Pro Ser Val Gly Gly Gly Thr Cys Asn Ser Leu Trp Tyr
100 105 110

acg aga gtt gtt caa gaa ata gtc ctg cat gaa aga tca gaa gag aaa 384
Thr Arg Val Val Gln Glu Ile Val Leu His Glu Arg Ser Glu Glu Lys
115 120 125

tgg aga gac tcc cga agt ggg aag ttc aca ttt cag gac gtg aga aaa 432
Trp Arg Asp Ser Arg Ser Gly Lys Phe Thr Phe Gln Asp Val Arg Lys
130 135 140

cgc tga 438
Arg *
145

<210> 248
<211> 145
<212> PRT
<213> Homo sapiens

<400> 248

Met Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Lys Trp
1 5 10 15

Lys Arg Arg Val Val Ser Gly His Leu Leu Ser Val Trp Cys Trp Ser
20 25 30

Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu Ser Leu Gly Asn
35 40 45

Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Glu Ala Ser Gly Leu
50 55 60

Ser Leu Gln Leu Gly Ile Lys Trp Thr Thr Glu Lys Pro Val Glu Asp
65 70 75 80

Ser Arg Ser Lys Glu Ile Thr Lys Ile Arg Asn Ala Ser Met Cys Thr
85 90 95

Gln Leu Pro Pro Ser Val Gly Gly Gly Thr Cys Asn Ser Leu Trp Tyr

100 105 110
 Thr Arg Val Val Gln Glu Ile Val Leu His Glu Arg Ser Glu Glu Lys
 115 120 125
 Trp Arg Asp Ser Arg Ser Gly Lys Phe Thr Phe Gln Asp Val Arg Lys
 130 135 140
 Arg
 145

<210> 249
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(552)

<400> 249
 atg aaa gtg gtg gtg gtg atg gtg gta ata ctg gtg gtg gtg aca ttg 48
 Met Lys Val Val Val Val Met Val Val Ile Leu Val Val Val Thr Leu
 1 5 10 15
 gtg gtg gtg gtg atg gtg gtg ata ctg gtg atg gtg gtg atg gtg gtg 96
 Val Val Val Val Met Val Val Ile Leu Val Met Val Val Met Val Val
 20 25 30
 gcg ctg gtg acc ctg aca tgg ggt cca gta gca gtg aca gtg gat gca 144
 Ala Leu Val Thr Leu Thr Trp Gly Pro Val Ala Val Thr Val Asp Ala
 35 40 45
 ggc tcc tgt ctc tca gca aac ctg ctg ggc gac agc gga ctc aga tgc 192
 Gly Ser Cys Leu Ser Ala Asn Leu Leu Gly Asp Ser Gly Leu Arg Cys
 50 55 60
 ctt ctg gaa tgt ctg ccg cag gtg ccc atc tcc ggt ttg ctt gac ctg 240
 Leu Leu Glu Cys Leu Pro Gln Val Pro Ile Ser Gly Leu Leu Asp Leu
 65 70 75 80
 ggc tct gag cag agc ttc cgg att cac ttc tcc aga gag gac cag gct 288
 Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln Ala
 85 90 95
 ggg aag aca ctc agg cta agt gag tgc agc ttc cgg cca gag cac gtg 336

Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu His Val
 100 105 110

tcc agg ctg gcc acc ggc ttg agc aag tcc ctg cag ctg acg gag ctc 384
 Ser Arg Leu Ala Thr Gly Leu Ser Lys Ser Leu Gln Leu Thr Glu Leu
 115 120 125

acg ctg acc cag tgc tgc ctg ggc cag aag cag ctg gcc atc ctc ctg 432
 Thr Leu Thr Gln Cys Cys Leu Gly Gln Lys Gln Leu Ala Ile Leu Leu
 130 135 140

agc ttg gtg ggg cga ccc gca ggg ctg ttc agc ctc aga gac aac tgc 480
 Ser Leu Val Gly Arg Pro Ala Gly Leu Phe Ser Leu Arg Asp Asn Cys
 145 150 155 160

aga gct aca aag aca gca cat cca caa atg gag acc atc aca tca tcg 528
 Arg Ala Thr Lys Thr Ala His Pro Gln Met Glu Thr Ile Thr Ser Ser
 165 170 175

aca ata gca gct tct gtt tac taa 552
 Thr Ile Ala Ala Ser Val Tyr *
 180

<210> 250

<211> 183

<212> PRT

<213> Homo sapiens

<400> 250

Met Lys Val Val Val Val Met Val Val Ile Leu Val Val Val Thr Leu
 1 5 10 15

Val Val Val Val Met Val Val Ile Leu Val Met Val Val Met Val Val
 20 25 30

Ala Leu Val Thr Leu Thr Trp Gly Pro Val Ala Val Thr Val Asp Ala
 35 40 45

Gly Ser Cys Leu Ser Ala Asn Leu Leu Gly Asp Ser Gly Leu Arg Cys
 50 55 60

Leu Leu Glu Cys Leu Pro Gln Val Pro Ile Ser Gly Leu Leu Asp Leu
 65 70 75 80

Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln Ala
 85 90 95

Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu His Val

65 70 75 80
 Trp Gly Glu Ile Ser Ile Asp Phe Val Glu Leu Gln Gly Lys Val Pro
 85 90 95
 Ser Ser Pro Ile Thr Lys Met Cys Thr His Asp Pro Leu Ala Lys Trp
 100 105 110
 Thr Leu Ser Pro Lys Ser Ser Asn Leu Lys Gln Met Asp Ala Arg Met
 115 120 125
 Glu Asn Ser Trp Asn Arg Leu Ile Ser Val Gly Ser Glu Arg Ala Ala
 130 135 140
 Thr Glu Leu Gly Glu Lys Ala Gln Leu Lys Arg Trp Lys Ile Tyr Ile
 145 150 155 160
 Ile Ser Val Ser Met Ser Ile Thr His Pro Glu Ile Gln Glu Arg Leu
 165 170 175
 Lys Asn Cys Leu Thr
 180

<210> 253
 <211> 426
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(426)

<400> 253

atg agg ccc cgg aaa gcc ttc ctg ctc ctg ctg ctc ttg ggg ctg gtg 48
 Met Arg Pro Arg Lys Ala Phe Leu Leu Leu Leu Leu Leu Gly Leu Val
 1 5 10 15

cag ctg ctg gcc gtg gcg ggt gcc gag ggc ccg gac gag ggg ctc cca 96
 Gln Leu Leu Ala Val Ala Gly Ala Glu Gly Pro Asp Glu Gly Leu Pro
 20 25 30

ctg tct tct ggc att tgc ttc cta aac tac aac cca gcc agc tcc act 144
 Leu Ser Ser Gly Ile Cys Phe Leu Asn Tyr Asn Pro Ala Ser Ser Thr
 35 40 45

gct tac ttc ttg gac att gtt gtc cag ccc ctt gga aaa cag ttg gaa 192
 Ala Tyr Phe Leu Asp Ile Val Val Gln Pro Leu Gly Lys Gln Leu Glu
 50 55 60

cag ccg ttg ggc tct gag caa caa ggc cct ttt att tca gtt aga tgc 240

Gln Pro Leu Gly Ser Glu Gln Gln Gly Pro Phe Ile Ser Val Arg Cys
65 70 75 80

tgg gct cgg gac ctg cag ccc gcc atg cct gag ctt ccc acc cac tcc 288
Trp Ala Arg Asp Leu Gln Pro Ala Met Pro Glu Leu Pro Thr His Ser
85 90 95

atg ggc tcc tgt gcg gcc cga gcc tcc ccg acg agc gcc acc ccc tgc 336
Met Gly Ser Cys Ala Ala Arg Ala Ser Pro Thr Ser Ala Thr Pro Cys
100 105 110

tcc acg gcg ccc agt ccc atc gac cac cca agg gct gag gag tgc gag 384
Ser Thr Ala Pro Ser Pro Ile Asp His Pro Arg Ala Glu Glu Cys Glu
115 120 125

cgc acg gcg cgg gac tgg cag cct gca gat ggc cta ctg tga 426
Arg Thr Ala Arg Asp Trp Gln Pro Ala Asp Gly Leu Leu *
130 135 140

<210> 254
<211> 141
<212> PRT
<213> Homo sapiens

<400> 254
Met Arg Pro Arg Lys Ala Phe Leu Leu Leu Leu Leu Gly Leu Val
1 5 10 15
Gln Leu Leu Ala Val Ala Gly Ala Glu Gly Pro Asp Glu Gly Leu Pro
20 25 30
Leu Ser Ser Gly Ile Cys Phe Leu Asn Tyr Asn Pro Ala Ser Ser Thr
35 40 45
Ala Tyr Phe Leu Asp Ile Val Val Gln Pro Leu Gly Lys Gln Leu Glu
50 55 60
Gln Pro Leu Gly Ser Glu Gln Gln Gly Pro Phe Ile Ser Val Arg Cys
65 70 75 80
Trp Ala Arg Asp Leu Gln Pro Ala Met Pro Glu Leu Pro Thr His Ser
85 90 95
Met Gly Ser Cys Ala Ala Arg Ala Ser Pro Thr Ser Ala Thr Pro Cys
100 105 110
Ser Thr Ala Pro Ser Pro Ile Asp His Pro Arg Ala Glu Glu Cys Glu
115 120 125
Arg Thr Ala Arg Asp Trp Gln Pro Ala Asp Gly Leu Leu

gag tat aca tat gct tgc tat ata aac tgc act gcc tct gcc gga att	432
Glu Tyr Thr Tyr Ala Cys Tyr Ile Asn Cys Thr Ala Ser Ala Gly Ile	
130 135 140	
gtc acc gag atg ctc agg cct ttc atc act ctt gtg tct aga gcc gcc	480
Val Thr Glu Met Leu Arg Pro Phe Ile Thr Leu Val Ser Arg Ala Ala	
145 150 155 160	
agg tgg tcc cag gac ccc ttt tca cct agc agt tcc gca gcc cat cgg	528
Arg Trp Ser Gln Asp Pro Phe Ser Pro Ser Ser Ser Ala Ala His Arg	
165 170 175	
caa tcc aca ccc cag atc cat ccc tgt atc gtg agc caa cct tcc tgc	576
Gln Ser Thr Pro Gln Ile His Pro Cys Ile Val Ser Gln Pro Ser Cys	
180 185 190	
aaa gtc ctc gtg ggc atc ggc atg tcc tat ttc tct ttc ctt ggg gca	624
Lys Val Leu Val Gly Ile Gly Met Ser Tyr Phe Ser Phe Leu Gly Ala	
195 200 205	
tcc tcg tca tta atg acc cca tcc gcg aca atc cta ccg ctg ctg tcc	672
Ser Ser Ser Leu Met Thr Pro Ser Ala Thr Ile Leu Pro Leu Leu Ser	
210 215 220	
tgc cgt gcg tct ctg acg gtg agc tta gtc agt cgt ctt cgc agt aga	720
Cys Arg Ala Ser Leu Thr Val Ser Leu Val Ser Arg Leu Arg Ser Arg	
225 230 235 240	
cac agc tcc cgg ata gct gct acc aag ttc gac gca tct ata tat cgc	768
His Ser Ser Arg Ile Ala Ala Thr Lys Phe Asp Ala Ser Ile Tyr Arg	
245 250 255	
tgc gcg tca gac gcc ggc gac aca cgc atc ttc cgt agt cat gcc ggg	816
Cys Ala Ser Asp Ala Gly Asp Thr Arg Ile Phe Arg Ser His Ala Gly	
260 265 270	
aga cgt cag ccg agc agt aca tat cgc gtt gta ccg aca atc cta agt	864
Arg Arg Gln Pro Ser Ser Thr Tyr Arg Val Val Pro Thr Ile Leu Ser	
275 280 285	
gca atc gat gtg gtt gtc gca agc tcc gtc aca agc tgc cgc gtc ttc	912
Ala Ile Asp Val Val Val Ala Ser Ser Val Thr Ser Cys Arg Val Phe	

290

295

300

gtg gct aac agc ggc gca tgt gcg ccc tga
 Val Ala Asn Ser Gly Ala Cys Ala Pro *
 305 310

942

<210> 256

<211> 313

<212> PRT

<213> Homo sapiens

<400> 256

Met Glu Asp Tyr Ile His Lys Leu Val Tyr Thr Val Phe Ala Cys Gly
 1 5 10 15
 Arg His Pro Ala Leu Leu Leu Leu Phe Val Pro Val Leu Pro Ser Ala
 20 25 30
 Gly Ser Ser Pro Leu Pro Gly His Val Leu Ser Ile Phe Ser Pro Pro
 35 40 45
 Ala Arg Ile Pro His Ala Arg Ser Val Ser Ser Gln Leu Phe Pro Tyr
 50 55 60
 Ala Ala Val Ala Ser Phe Gly Pro Ser Leu Arg Val Val Glu Phe Leu
 65 70 75 80
 Glu Arg Leu Leu Leu Val Arg Ala Ala Asp Arg Ser Cys Arg Ser Arg
 85 90 95
 Phe Ala Pro Ile Arg Asp Arg Gly Leu Arg Ser Ser Arg Cys Arg Thr
 100 105 110
 Asp Leu Arg Val Ser Gly Trp His Gly Leu Pro Leu Asp Leu Pro Lys
 115 120 125
 Glu Tyr Thr Tyr Ala Cys Tyr Ile Asn Cys Thr Ala Ser Ala Gly Ile
 130 135 140
 Val Thr Glu Met Leu Arg Pro Phe Ile Thr Leu Val Ser Arg Ala Ala
 145 150 155 160
 Arg Trp Ser Gln Asp Pro Phe Ser Pro Ser Ser Ser Ala Ala His Arg
 165 170 175
 Gln Ser Thr Pro Gln Ile His Pro Cys Ile Val Ser Gln Pro Ser Cys
 180 185 190
 Lys Val Leu Val Gly Ile Gly Met Ser Tyr Phe Ser Phe Leu Gly Ala
 195 200 205
 Ser Ser Ser Leu Met Thr Pro Ser Ala Thr Ile Leu Pro Leu Leu Ser
 210 215 220
 Cys Arg Ala Ser Leu Thr Val Ser Leu Val Ser Arg Leu Arg Ser Arg
 225 230 235 240

T00250.f22560

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<210> 257
<211> 291
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(291)
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<400> 257																
atg	ctt	tgg	ctc	ctt	ttg	gct	ctt	ttt	gcc	ccg	ggt	cgg	gcg	ggg	ggc	48
Met	Leu	Trp	Leu	Leu	Leu	Ala	Leu	Phe	Ala	Pro	Gly	Arg	Ala	Gly	Gly	
1			5			10			15							
ggg	ggg	tgg	ggg	tgc	atc	ttc	cct	gat	aca	cca	cac	tct	cca	ttc	cct	96
Gly	Gly	Trp	Gly	Cys	Ile	Phe	Pro	Asp	Thr	Pro	His	Ser	Pro	Phe	Pro	
			20			25						30				
ggg	ata	tat	gac	act	gat	tgg	gct	acc	acg	atc	ggg	gac	tcc	aca	cca	144
Gly	Ile	Tyr	Asp	Thr	Asp	Trp	Ala	Thr	Thr	Ile	Gly	Asp	Ser	Thr	Pro	
35						40						45				
cta	cta	tgg	ccc	ttc	att	tct	gtg	gct	ctg	tgc	tcc	tcc	agt	gca	ctt	192
Leu	Leu	Trp	Pro	Phe	Ile	Ser	Val	Ala	Leu	Cys	Ser	Ser	Ser	Ala	Leu	
50						55						60				
cct	gca	ggg	cac	ccg	gca	ttc	ccc	aat	cct	aga	cgc	tac	gca	gat	gcc	240
Pro	Ala	Gly	His	Pro	Ala	Phe	Pro	Asn	Pro	Arg	Arg	Tyr	Ala	Asp	Ala	
65						70			75			80				
agc	cat	gca	gaa	tca	cat	acc	atc	tta	cct	gct	gag	ctc	tcc	cct	ttg	288
Ser	His	Ala	Glu	Ser	His	Thr	Ile	Leu	Pro	Ala	Glu	Leu	Ser	Pro	Leu	

260

85

90

95

tga

*

291

<210> 258

<211> 96

<212> PRT

<213> Homo sapiens

<400> 258

Met Leu Trp Leu Leu Leu Ala Leu Phe Ala Pro Gly Arg Ala Gly Gly
1 5 10 15
Gly Gly Trp Gly Cys Ile Phe Pro Asp Thr Pro His Ser Pro Phe Pro
20 25 30
Gly Ile Tyr Asp Thr Asp Trp Ala Thr Thr Ile Gly Asp Ser Thr Pro
35 40 45
Leu Leu Trp Pro Phe Ile Ser Val Ala Leu Cys Ser Ser Ser Ala Leu
50 55 60
Pro Ala Gly His Pro Ala Phe Pro Asn Pro Arg Arg Tyr Ala Asp Ala
65 70 75 80
Ser His Ala Glu Ser His Thr Ile Leu Pro Ala Glu Leu Ser Pro Leu
85 90 95

<210> 259

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(231)

<400> 259

atg aaa ctc atg gaa aca ctt aac cag tgc ata aac gct ggt cat gaa 48
Met Lys Leu Met Glu Thr Leu Asn Gln Cys Ile Asn Ala Gly His Glu
1 5 10 15

atg acg aag gct atc gcc att gca cag ttt aat gat gac agc ccg gaa 96
Met Thr Lys Ala Ile Ala Ile Ala Gln Phe Asn Asp Asp Ser Pro Glu
20 25 30

ggt ggg gtt tct tct cag gct atc aga gat gcc gag aaa gca ggg cga 192
Val Gly Val Ser Ser Gln Ala Ile Arg Asp Ala Glu Lys Ala Gly Arg

50 55 60

cta ccg cac ccg gat atg gaa att cga gga cgg tgt tga 231
Leu Pro His Pro Asp Met Glu Ile Arg Gly Arg Cys *
65 70 75

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<210> 260
<211> 76
<212> PRT
<213> Homo sapiens
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<400> 260
Met Lys Leu Met Glu Thr Leu Asn Gln Cys Ile Asn Ala Gly His Glu
1 5 10 15
Met Thr Lys Ala Ile Ala Ile Ala Gln Phe Asn Asp Asp Ser Pro Glu
20 25 30
Ala Arg Lys Ile Thr Arg Arg Trp Arg Ile Gly Glu Ala Ala Asp Leu
35 40 45
Val Gly Val Ser Ser Gln Ala Ile Arg Asp Ala Glu Lys Ala Gly Arg
50 55 60
Leu Pro His Pro Asp Met Glu Ile Arg Gly Arg Cys
65 70 75

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<210> 261
<211> 375
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(375)

<400> 261
atg aag ttc ctg ctc ctg gtc ttg gca gcc ctc gga ttc ctg acc cag 48
Met Lys Phe Leu Leu Leu Val Leu Ala Ala Leu Gly Phe Leu Thr Gln

<210> 262
<211> 124
<212> PRT
<213> Homo sapiens

<400> 262

Met	Lys	Phe	Leu	Leu	Val	Leu	Ala	Ala	Leu	Gly	Phe	Leu	Thr	Gln	
1			5				10					15			
Val	Ile	Pro	Gly	Ala	Asp	Ser	Ala	Val	Lys	Cys	Ala	Pro	Gly	Asp	Ser
			20				25					30			
Arg	Pro	Gly	Arg	Ile	Pro	His	Arg	Ser	Pro	Thr	Pro	Arg	Ser	Pro	Pro
		35					40					45			

Ser Arg Leu Ile Asp Leu Cys Gln Ser Leu Pro Pro Ser Ala Gly Ser
 50 55 60
 Thr Arg Tyr Thr Arg Ala Leu Glu Val Ala Arg Ala Gly Gln Thr Gly
 65 70 75 80
 Ala Pro Asp Thr Phe Gln Gly Pro Ala Lys Asp Leu Pro Met Ser Thr
 85 90 95
 Gly Val Pro Asp Thr Arg Asp Pro Gly Gln Asp Ser His Phe Thr Arg
 100 105 110
 Tyr Thr Asp Thr Gly Leu Arg Glu Gln Glu Ile Pro
 115 120

<210> 263
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(420)

<400> 263

atg aaa gag gca ttg acc aac cag aca cca atg act caa caa ctt gat 48
 Met Lys Glu Ala Leu Thr Asn Gln Thr Pro Met Thr Gln Gln Leu Asp
 1 5 10 15

att agc ctg att tta ctg atg gcc act tgg gaa ctg gtg caa gga gtg 96
 Ile Ser Leu Ile Leu Leu Met Ala Thr Trp Glu Leu Val Gln Gly Val
 20 25 30

cag agg att cga gta tca ctt att gtt ctt cct gat gac cca ctg gag 144
 Gln Arg Ile Arg Val Ser Leu Ile Val Leu Pro Asp Asp Pro Leu Glu
 35 40 45

gac ttg cgc ttc tat tct tac aca ttt gtg tcc ttt gga gtt aga gtt 192
 Asp Leu Arg Phe Tyr Ser Tyr Thr Phe Val Ser Phe Gly Val Arg Val
 50 55 60

cat ggt tct act ctt gcc ata cga cac att aaa ata caa gct atg gct 240
 His Gly Ser Thr Leu Ala Ile Arg His Ile Lys Ile Gln Ala Met Ala
 65 70 75 80

gct gct ggc cac ttt gaa ttc cat ctt ggc aga gaa gtc cgt gaa ggt 288
 Ala Ala Gly His Phe Glu Phe His Leu Gly Arg Glu Val Arg Glu Gly

85

90

95

cac tta gaa gtt att ttc caa aca tgc aat gga aag tgt atc tct gtg 336
 His Leu Glu Val Ile Phe Gln Thr Cys Asn Gly Lys Cys Ile Ser Val
 100 105 110

act aaa caa gtg gac tgt ggt ggc cat agt aga gca cga ctc aga ttg 384
 Thr Lys Gln Val Asp Cys Gly Gly His Ser Arg Ala Arg Leu Arg Leu
 115 120 125

tcc tct gaa aaa acc tgc tgt aga aag cat att tga 420
 Ser Ser Glu Lys Thr Cys Cys Arg Lys His Ile *
 130 135

<210> 264

<211> 139

<212> PRT

<213> Homo sapiens

<400> 264

Met Lys Glu Ala Leu Thr Asn Gln Thr Pro Met Thr Gln Gln Leu Asp
 1 5 10 15
 Ile Ser Leu Ile Leu Leu Met Ala Thr Trp Glu Leu Val Gln Gly Val
 20 25 30
 Gln Arg Ile Arg Val Ser Leu Ile Val Leu Pro Asp Asp Pro Leu Glu
 35 40 45
 Asp Leu Arg Phe Tyr Ser Tyr Thr Phe Val Ser Phe Gly Val Arg Val
 50 55 60
 His Gly Ser Thr Leu Ala Ile Arg His Ile Lys Ile Gln Ala Met Ala
 65 70 75 80
 Ala Ala Gly His Phe Glu Phe His Leu Gly Arg Glu Val Arg Glu Gly
 85 90 95
 His Leu Glu Val Ile Phe Gln Thr Cys Asn Gly Lys Cys Ile Ser Val
 100 105 110
 Thr Lys Gln Val Asp Cys Gly Gly His Ser Arg Ala Arg Leu Arg Leu
 115 120 125
 Ser Ser Glu Lys Thr Cys Cys Arg Lys His Ile
 130 135

<210> 265

<211> 477

<212> DNA

T00230#226800

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(477)

<400> 265

atg ttt tat tgg ttg gtg caa cgg gta gcc tgt gtt tta ctg tta act	48
Met Phe Tyr Trp Leu Val Gln Arg Val Ala Cys Val Leu Leu Leu Thr	
1 5 10 15	
gca atg ctt ttt caa acg gat gct ttt gaa aca ccc tgg aat ata gtt	96
Ala Met Leu Phe Gln Thr Asp Ala Phe Glu Thr Pro Trp Asn Ile Val	
20 25 30	
ggc aga atg aat aaa gga atg aat aaa agc att gtt cac ata atg cga	144
Gly Arg Met Asn Lys Gly Met Asn Lys Ser Ile Val His Ile Met Arg	
35 40 45	
tat aac ttt cta gaa ggt caa att aac cct act ttc gat gta gaa atg	192
Tyr Asn Phe Leu Glu Gly Gln Ile Asn Pro Thr Phe Asp Val Glu Met	
50 55 60	
act aac ata acc gaa gat cta atg gtg atg tgg tca tgc aca cag tgt	240
Thr Asn Ile Thr Glu Asp Leu Met Val Met Trp Ser Cys Thr Gln Cys	
65 70 75 80	
gta ggt gct acc aac tgt tgc aga cac agt tca tct cag aac aga aag	288
Val Gly Ala Thr Asn Cys Cys Arg His Ser Ser Ser Gln Asn Arg Lys	
85 90 95	
cat gaa act cta gcc aca gga atc aga atc ctt ctt ccc caa ggg tca	336
His Glu Thr Leu Ala Thr Gly Ile Arg Ile Leu Leu Pro Gln Gly Ser	
100 105 110	
atc act cat tcc cca gct gct gaa agt gtg gct gcc aat tgt tta cag	384
Ile Thr His Ser Pro Ala Ala Glu Ser Val Ala Ala Asn Cys Leu Gln	
115 120 125	
ctg tat cct tct ctc aag cat tac tct cag tct ctg gga gcc aag tct	432
Leu Tyr Pro Ser Leu Lys His Tyr Ser Gln Ser Leu Gly Ala Lys Ser	
130 135 140	

tct gga aat gtc tgg gag gct ata cta gga agg aga ggg tgg tag
 Ser Gly Asn Val Trp Glu Ala Ile Leu Gly Arg Arg Gly Trp *
 145 150 155

477

<210> 266
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 266

Met Phe Tyr Trp Leu Val Gln Arg Val Ala Cys Val Leu Leu Leu Thr
 1 5 10 15
 Ala Met Leu Phe Gln Thr Asp Ala Phe Glu Thr Pro Trp Asn Ile Val
 20 25 30
 Gly Arg Met Asn Lys Gly Met Asn Lys Ser Ile Val His Ile Met Arg
 35 40 45
 Tyr Asn Phe Leu Glu Gly Gln Ile Asn Pro Thr Phe Asp Val Glu Met
 50 55 60
 Thr Asn Ile Thr Glu Asp Leu Met Val Met Trp Ser Cys Thr Gln Cys
 65 70 75 80
 Val Gly Ala Thr Asn Cys Cys Arg His Ser Ser Ser Gln Asn Arg Lys
 85 90 95
 His Glu Thr Leu Ala Thr Gly Ile Arg Ile Leu Leu Pro Gln Gly Ser
 100 105 110
 Ile Thr His Ser Pro Ala Ala Glu Ser Val Ala Ala Asn Cys Leu Gln
 115 120 125
 Leu Tyr Pro Ser Leu Lys His Tyr Ser Gln Ser Leu Gly Ala Lys Ser
 130 135 140
 Ser Gly Asn Val Trp Glu Ala Ile Leu Gly Arg Arg Gly Trp
 145 150 155

<210> 267
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(603)

<400> 267

atg gct gca gct tgg acc gtg gtg ctg gtg act ttg gtg cta ggc ttg

48

576

603

$\langle 400 \rangle$ 268

<210> 269

<211> 624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(624)

<400> 269

atg gga aga atc ccg gta att ctg ctg ctg gct gcc ccc cct gtc tcc	48
Met Gly Arg Ile Pro Val Ile Leu Leu Leu Ala Ala Pro Pro Val Ser	
1 5 10 15	

ctg tca gcg gtg cga cta gct act agt agt agg agg act aag cca cta	96
Leu Ser Ala Val Arg Leu Ala Thr Ser Ser Arg Arg Thr Lys Pro Leu	
20 25 30	

acg agc ttc ctc gct ctg cag aaa cgt ttg ggc ctc gtc cca tcg gcg	144
Thr Ser Phe Leu Ala Leu Gln Lys Arg Leu Gly Leu Val Pro Ser Ala	
35 40 45	

gac tat atg cag tat ctc cct att gta cgt cgg ggc agg cag cat agc	192
Asp Tyr Met Gln Tyr Leu Pro Ile Val Arg Arg Gly Arg Gln His Ser	
50 55 60	

att gtg gcg tcc acc cag acg ggc cgg gct tcg gta gtg act gct act	240
Ile Val Ala Ser Thr Gln Thr Gly Arg Ala Ser Val Val Thr Ala Thr	
65 70 75 80	

tac tct ggc gcg cgc gat atc tca ggc atc agt ttt cga acc agg gct	288
Tyr Ser Gly Ala Arg Asp Ile Ser Gly Ile Ser Phe Arg Thr Arg Ala	
85 90 95	

cat aga gcc ctc gga tat tta ctt cac aga gtt ttt atg agg ata gct	336
His Arg Ala Leu Gly Tyr Leu Leu His Arg Val Phe Met Arg Ile Ala	
100 105 110	

ttt gat aga agc tgc agg agc ctg cgc gtc atc cga gat gcc cac ggg	384
Phe Asp Arg Ser Cys Arg Ser Leu Arg Val Ile Arg Asp Ala His Gly	
115 120 125	

ggt ctt cct tac ctt cag gtg gaa tgc cac ccc agg gac aac cct cct	432
Gly Leu Pro Tyr Leu Gln Val Glu Cys His Pro Arg Asp Asn Pro Pro	

130	135	140	
gtg gag tac ttg ttc cta cac ctt ggt tgg cga gag caa acc gat gca			480
Val Glu Tyr Leu Phe Leu His Leu Gly Trp Arg Glu Gln Thr Asp Ala			
145	150	155	160
ggc gtt tct aaa aca aat gag ccc tgg gag agc cct gaa cgc att tat			528
Gly Val Ser Lys Thr Asn Glu Pro Trp Glu Ser Pro Glu Arg Ile Tyr			
	165	170	175
tat gag cct cga ggg act ggg aag ctg cag aga ccc aaa gct gtc cga			576
Tyr Glu Pro Arg Gly Thr Gly Lys Leu Gln Arg Pro Lys Ala Val Arg			
	180	185	190
gag gac ttg gga ctt gct ctg caa aag acc tgg cct ctg ctt ttt tga			624
Glu Asp Leu Gly Leu Ala Leu Gln Lys Thr Trp Pro Leu Leu Phe *			
	195	200	205

<210> 270

<211> 207

<212> PRT

<213> Homo sapiens

<400> 270

Met Gly Arg Ile Pro Val Ile Leu Leu Leu Ala Ala Pro Pro Val Ser	
1 5 10 15	
Leu Ser Ala Val Arg Leu Ala Thr Ser Ser Arg Arg Thr Lys Pro Leu	
20 25 30	
Thr Ser Phe Leu Ala Leu Gln Lys Arg Leu Gly Leu Val Pro Ser Ala	
35 40 45	
Asp Tyr Met Gln Tyr Leu Pro Ile Val Arg Arg Gly Arg Gln His Ser	
50 55 60	
Ile Val Ala Ser Thr Gln Thr Gly Arg Ala Ser Val Val Thr Ala Thr	
65 70 75 80	
Tyr Ser Gly Ala Arg Asp Ile Ser Gly Ile Ser Phe Arg Thr Arg Ala	
85 90 95	
His Arg Ala Leu Gly Tyr Leu Leu His Arg Val Phe Met Arg Ile Ala	
100 105 110	
Phe Asp Arg Ser Cys Arg Ser Leu Arg Val Ile Arg Asp Ala His Gly	
115 120 125	
Gly Leu Pro Tyr Leu Gln Val Glu Cys His Pro Arg Asp Asn Pro Pro	
130 135 140	

ctg act gat act gcc atg gta cta gtc act gac atc gtg atg cgt gct 864
 Leu Thr Asp Thr Ala Met Val Leu Val Thr Asp Ile Val Met Arg Ala
 275 280 285

gta ctc gtc act ctg cat gcg tga 888
 Val Leu Val Thr Leu His Ala *
 290 295

<210> 272
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 272

Met Ala Gly Leu Leu Ser Pro Ile Leu Leu Met Leu Leu Ala Leu Val
 1 5 10 15
 Asn Val Arg Thr Gln Thr Pro Arg Thr Asn Thr Leu Ile Asp Cys Ala
 20 25 30
 Pro Gly Trp Ala Leu Lys Asp Arg Ser Val Gly Ser Gly Ser Thr Ser
 35 40 45
 Met Leu Ala Ala Gln His Ile Ala Tyr Pro Gly Tyr Gln Val Leu Ile
 50 55 60
 Leu Glu Arg Leu Met Pro Leu Thr Thr Asp Ser Arg Leu Phe Trp Ser
 65 70 75 80
 Thr Asp Lys Trp Ile Val Arg Gly Glu Pro Tyr Leu Arg Met Arg Ser
 85 90 95
 Phe Ala Tyr Arg Ile Thr Cys Pro Lys Leu Lys Ser Tyr Glu Gln Gln
 100 105 110
 Leu Tyr Glu Ala Leu Gln Arg Leu Val Thr Glu Ser Asn Gln His Leu
 115 120 125
 Lys Val Arg His Val Arg Ser Lys Trp His Leu Tyr Val Ser Thr Arg
 130 135 140
 Leu Ser Arg Arg His Arg Thr Ala Gln Asp Val Cys Ile Gly Asp Ala
 145 150 155 160
 Ala Leu Thr Gly Tyr Gly Leu Asp Ala Arg Thr Arg Thr Lys Thr His
 165 170 175
 Met Tyr Cys Val Asp Thr Tyr Ser Asp Leu Lys Ala Met Val Ser Thr
 180 185 190
 Leu Val Arg Ile Val Ser Asp Ser Arg Val Asp Pro Tyr Arg Ile Val
 195 200 205
 Tyr Arg Leu Arg Ile Arg Ile Arg Met Arg Ser Ala Leu Thr Arg Leu


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<210> 274
<211> 192
<212> PRT
<213> Homo sapiens

      <400> 274
Met Leu Leu Ile Glu Leu Gly Leu Ala Asp Arg Val Trp Ala Arg Ser
 1             5             10             15
Cys Val Cys Gly Leu Pro Ala Ala Gln Gln Gly Ala Gly Trp Thr Ser
          20          25          30
Glu Ala Met Lys Pro Arg Ser His Gly Leu Val Thr Gly Phe Gln Gly

```


35 40 45
 Thr Gln Gln Thr Val Lys Ala Leu Gln Ile Gln Arg Arg Pro Ala Gly
 50 55 60
 Phe Glu Pro Ala Met Gln Gly Asn Leu Gln Gly Ser Leu Arg Ile Gly
 65 70 75 80
 His Cys His Cys Pro Leu Gly Ala Asp Glu Gly Ser Asp Leu Pro Glu
 85 90 95
 Val Thr Val Leu Val Arg Asp Gly Ser Arg Thr Pro His Pro Gly Val
 100 105 110
 Tyr Pro Gly Trp Tyr His Arg Pro Val Arg Gly Leu Val Asn Met Lys
 115 120 125
 Val Pro Phe Val Arg Pro Leu His Glu Asp Pro Asn Pro Leu Lys Ile
 130 135 140
 Phe Met Leu Ser Ala Ala Gly Asn Lys Ser Arg Trp Ile Pro Gly Ser
 145 150 155 160
 Leu Cys Leu His Val Thr Ala Thr Pro Thr Thr Ala Glu Leu Pro Gly
 165 170 175
 Ala Ser Arg Asp Gly Lys Val Pro Ala Val Cys Arg Val Pro Ala Val
 180 185 190

<210> 275
 <211> 510
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(510)

<400> 275

atg agg tca gaa gcc ttg ctg cta tat ttc aca ctg cta cac ttt gct 48
 Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
 1 5 10 15

ggg gct ggt ttc cca gaa gat tct gag cca atc agt att tcg cat ggc 96
 Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
 20 25 30

aac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg 144
 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
 35 40 45

aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg 192

35 40 45
 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 50 55 60
 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Thr Gln Arg Gly Phe Val Val
 65 70 75 80
 Phe Val Val Thr Gly Ser Thr Leu His Arg Cys Leu Leu Ile Thr Ser
 85 90 95
 Leu Trp Arg Gln Thr His Pro Ser Tyr His Ser Ser Ser Glu Thr Gly
 100 105 110
 Arg Pro Val Lys Gly Gly Glu Arg Gly Lys Cys Thr Leu Asn His Phe
 115 120 125
 Glu Leu Gly Tyr Trp Leu Pro Val Ser Tyr Thr Leu Arg Val Val Ile
 130 135 140
 Gly Val Gly Thr Leu Glu Tyr Ala Tyr Ser Ser Ser Lys Lys Lys Gln
 145 150 155 160
 Ser Trp His Tyr Cys Glu Lys Ser Thr
 165

<210> 277

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(423)

<400> 277

atg tcc acc acc aca tgc caa gtg gtg gcg ttc ctc ctg tcc atc ctg 48
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
 1 5 10 15

ggg ctg gcc ggc tgc atc gcg gcc acc ggg atg gac atg tgg agc acc 96
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20 25 30

cag gac ctg tac gac aac ccc gtc acc tcc gtg ttc cag tac gaa ggg 144
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35 40 45

ctc tgg agg agc tgc gtg agg cag agt tca ggc ttc acc gaa tgc agg 192
 Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50 55 60

115 120 125
 Ser Thr Ser Leu Cys Thr Lys Pro Arg Ala Phe Ser
 130 135 140

<210> 279
 <211> 333
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(333)

<400> 279

atg atg ctg ctg ttg ctg tgt ctg ggg ttg acc ctc gtc tgt gcc cag 48
 Met Met Leu Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys Ala Gln
 1 5 10 15

gag gaa gaa aac aat gat gct gtg aca agc aac ttc gat ctg tca aag 96
 Glu Glu Glu Asn Asn Asp Ala Val Thr Ser Asn Phe Asp Leu Ser Lys
 20 25 30

cac att gct cag gat ata gca tca att cga aca ccg gat gtg agc tca 144
 His Ile Ala Gln Asp Ile Ala Ser Ile Arg Thr Pro Asp Val Ser Ser
 35 40 45

caa ctc aag gag agg ttt gtg aaa tat tgt gaa gaa cat ggg att gat 192
 Gln Leu Lys Glu Arg Phe Val Lys Tyr Cys Glu Glu His Gly Ile Asp
 50 55 60

aag gaa aac ata ttt gac ttg acc aaa gtt gga ttc tct gct gaa atc 240
 Lys Glu Asn Ile Phe Asp Leu Thr Lys Val Gly Phe Ser Ala Glu Ile
 65 70 75 80

atg cgg gcc gat tcg cgg tct cga tgt tta acc gtg ctg gta aca cca 288
 Met Arg Ala Asp Ser Arg Ser Arg Cys Leu Thr Val Leu Val Thr Pro
 85 90 95

aac ctc gat gct tgc gac gac ttg gtg cac ata ttg ttc gac tag 333
 Asn Leu Asp Ala Cys Asp Asp Leu Val His Ile Leu Phe Asp *
 100 105 110

<210> 280
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 280
 Met Met Leu Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys Ala Gln
 1 5 10 15
 Glu Glu Glu Asn Asn Asp Ala Val Thr Ser Asn Phe Asp Leu Ser Lys
 20 25 30
 His Ile Ala Gln Asp Ile Ala Ser Ile Arg Thr Pro Asp Val Ser Ser
 35 40 45
 Gln Leu Lys Glu Arg Phe Val Lys Tyr Cys Glu Glu His Gly Ile Asp
 50 55 60
 Lys Glu Asn Ile Phe Asp Leu Thr Lys Val Gly Phe Ser Ala Glu Ile
 65 70 75 80
 Met Arg Ala Asp Ser Arg Ser Arg Cys Leu Thr Val Leu Val Thr Pro
 85 90 95
 Asn Leu Asp Ala Cys Asp Asp Leu Val His Ile Leu Phe Asp
 100 105 110

<210> 281
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(471)

<400> 281
 atg aaa ata agc tgc tca gat ctt ctg ctg cag gga gca aag ttg atg 48
 Met Lys Ile Ser Cys Ser Asp Leu Leu Leu Gln Gly Ala Lys Leu Met
 1 5 10 15
 atg gtt cca gct gac tcc ctt ctg gat tta ctg ctg tta acc tgc ctt 96
 Met Val Pro Ala Asp Ser Leu Leu Asp Leu Leu Leu Leu Thr Cys Leu
 20 25 30
 cct cag gca gga gag tct cga gta gaa ggc aaa gat acc cct gcc tcg 144
 Pro Gln Ala Gly Glu Ser Arg Val Glu Gly Lys Asp Thr Pro Ala Ser
 35 40 45

Ile Asn Pro Arg Phe Asn Leu Gly Gly Ser Asp Ala Phe Leu Val Ser
 65 70 75 80
 Pro Ile Arg Gln Asp Leu Arg Gly Gln Val Leu Ser Ile Phe Glu Leu
 85 90 95
 Thr Gln Ser Thr Leu Ser Asp Glu Arg Ile Thr Gln His Gln His Leu
 100 105 110
 His Ser Arg Gly Glu Leu Ser Cys Glu Pro Asp Val Glu Pro Leu Gly
 115 120 125
 Phe Ser Ala Arg Lys Gly Gln Cys Leu Arg Arg Asp His Ser Gln Ile
 130 135 140
 Ala Thr Pro Pro Ser Val Asn Ala Glu Lys Thr Thr
 145 150 155

<210> 283
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(702)

<400> 283

atg gaa ggc tcc att tat gct tgg ggc att ctc ttg atg ttg ggc gcg	48
Met Glu Gly Ser Ile Tyr Ala Trp Gly Ile Leu Leu Met Leu Gly Ala	
1 5 10 15	
ggt cct ccg ggg tgg tgt ggg ggt gtg ttg aaa tct gct cga cgt ccg	96
Val Pro Pro Gly Trp Cys Gly Gly Val Leu Lys Ser Ala Arg Arg Pro	
20 25 30	
gag aag gct acg gcc gtt gtg cta cat gag gag tgt atg cgt aaa cat	144
Glu Lys Ala Thr Ala Val Val Leu His Glu Glu Cys Met Arg Lys His	
35 40 45	
ctt gcg gct aaa ccg acc gct cta att tta aaa agg cat cgg caa gca	192
Leu Ala Ala Lys Pro Thr Ala Leu Ile Leu Lys Arg His Arg Gln Ala	
50 55 60	
ggc gcc cac aag tcg agt tac ccg ggt caa caa agc tca gcg cct acc	240
Gly Ala His Lys Ser Ser Tyr Pro Gly Gln Gln Ser Ser Ala Pro Thr	
65 70 75 80	

atg aaa gta agc cgg ttc acc aga ccc cag ccc agt ctc caa gtt gca 336
Met Lys Val Ser Arg Phe Thr Arg Pro Gln Pro Ser Leu Gln Val Ala
100 105 110

cag cat gta aat tca gcc acc aag ttc ccc tgc agg gct ttt ggg acc 384
Gln His Val Asn Ser Ala Thr Lys Phe Pro Cys Arg Ala Phe Gly Thr
115 120 125

tat ctt cag gtg gtc gac aag gct tgg aac tct cgc tgg cag act agt 432
Tyr Leu Gln Val Val Asp Lys Ala Trp Asn Ser Arg Trp Gln Thr Ser
130 135 140

att gtc ata ata cct gga ccc acg ggc atg aac gcc tca cca tca cat 480
Ile Val Ile Ile Pro Gly Pro Thr Gly Met Asn Ala Ser Pro Ser His
145 150 155 160

ccg agt cag ctt tgc gcg gcg tct gaa tcg gtc cgg cat cgg tta cgc 528
Pro Ser Gln Leu Cys Ala Ala Ser Glu Ser Val Arg His Arg Leu Arg
165 170 175

att ggg cgc ctg ccc gcc gcc aag ggt tta gct tcg ctc atg tca aga 576
Ile Gly Arg Leu Pro Ala Ala Lys Gly Leu Ala Ser Leu Met Ser Arg
180 185 190

cgt ctt cgt ccg atg act gga act aca gct gaa gtg tcg tca aaa atc 624
Arg Leu Arg Pro Met Thr Gly Thr Thr Ala Glu Val Ser Ser Lys Ile
195 200 205

atc agg gat ggg gga gca gaa cgt ccc ggg gga ccg cgg ctc cca act 672
Ile Arg Asp Gly Gly Ala Glu Arg Pro Gly Gly Pro Arg Leu Pro Thr
210 215 220

cac gtt gct ccc act ccg aga ctc aag taa 702
His Val Ala Pro Thr Pro Arg Leu Lys *
225 230

 $\langle 211 \rangle$ 233

<212> PRT

<213> Homo sapiens

<400> 284

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Met Glu Gly Ser Ile Tyr Ala Trp Gly Ile Leu Leu Met Leu Gly Ala
 1          5          10          15
Val Pro Pro Gly Trp Cys Gly Gly Val Leu Lys Ser Ala Arg Arg Pro
          20          25          30
Glu Lys Ala Thr Ala Val Val Leu His Glu Glu Cys Met Arg Lys His
          35          40          45
Leu Ala Ala Lys Pro Thr Ala Leu Ile Leu Lys Arg His Arg Gln Ala
          50          55          60
Gly Ala His Lys Ser Ser Tyr Pro Gly Gln Gln Ser Ser Ala Pro Thr
65          70          75          80
Phe Glu Arg Gly Arg Leu Arg Ile Gly Ala Pro Ala Thr Pro Gln Tyr
          85          90          95
Met Lys Val Ser Arg Phe Thr Arg Pro Gln Pro Ser Leu Gln Val Ala
          100          105          110
Gln His Val Asn Ser Ala Thr Lys Phe Pro Cys Arg Ala Phe Gly Thr
          115          120          125
Tyr Leu Gln Val Val Asp Lys Ala Trp Asn Ser Arg Trp Gln Thr Ser
          130          135          140
Ile Val Ile Ile Pro Gly Pro Thr Gly Met Asn Ala Ser Pro Ser His
          145          150          155          160
Pro Ser Gln Leu Cys Ala Ala Ser Glu Ser Val Arg His Arg Leu Arg
          165          170          175
Ile Gly Arg Leu Pro Ala Ala Lys Gly Leu Ala Ser Leu Met Ser Arg
          180          185          190
Arg Leu Arg Pro Met Thr Gly Thr Thr Ala Glu Val Ser Ser Lys Ile
          195          200          205
Ile Arg Asp Gly Gly Ala Glu Arg Pro Gly Gly Pro Arg Leu Pro Thr
          210          215          220
His Val Ala Pro Thr Pro Arg Leu Lys
225          230

```

<210> 285

<211> 369

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(369)

Met Pro Cys Ala Leu Trp Glu His Lys Asn Lys Val Arg Leu Ser Pro
1 5 10 15

Leu Ser Ser Leu Leu Leu Leu Leu His Pro Gly Tyr Gly Gly Gln Ser
 20 25 30
 Glu Ser Glu Ser Leu Gln Gln Asn Gly Trp Leu Tyr Leu Ile Leu Glu
 35 40 45
 Gly Ile Tyr Phe Leu Lys Val Gln Ala Trp Val Ile Pro Asn Asp Asn
 50 55 60
 Leu Asn Arg Met Leu Leu Ala Glu Val Asn Lys Tyr Glu Asn Val Leu
 65 70 75 80
 Val Ile Lys Val Leu Gly Glu Leu His Gly Thr Pro Lys Ser Ala Tyr
 85 90 95
 Glu Lys Val Trp Gly Ile Ala Asp Ser Asn Gln Asn Gln Lys Cys Thr
 100 105 110
 Cys Ser Asp Tyr Pro Tyr Lys Gln Leu Lys
 115 120

<210> 287

<211> 486

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(486)

<400> 287

atg ggg aaa ctc ttg act ttg gtc agc atg ctc cta agt gga ctg cag 48
 Met Gly Lys Leu Leu Thr Leu Val Ser Met Leu Leu Ser Gly Leu Gln
 1 5 10 15

gct atg tgg gaa ctg gtg tat aga act att ggg cac caa ctt cac tgg 96
 Ala Met Trp Glu Leu Val Tyr Arg Thr Ile Gly His Gln Leu His Trp
 20 25 30

atc agt ggc tat ata gcg acg gtt gta cga ggg ttt cgc cac gtc aca 144
 Ile Ser Gly Tyr Ile Ala Thr Val Val Arg Gly Phe Arg His Val Thr
 35 40 45

caa ggt gat tgc aaa cat tat gtg atc ctc aca aac aca ggt tgt atc 192
 Gln Gly Asp Cys Lys His Tyr Val Ile Leu Thr Asn Thr Gly Cys Ile
 50 55 60

tgt ggt gga caa gtt atg tgg act gta cct tat tgt tat cct ggt gtg 240
 Cys Gly Gly Gln Val Met Trp Thr Val Pro Tyr Cys Tyr Pro Gly Val

<210> 288
<211> 161
<212> PRT
<213> Homo sapiens

<400> 288

Met	Gly	Lys	Leu	Leu	Thr	Leu	Val	Ser	Met	Leu	Leu	Ser	Gly	Leu	Gln
1			5					10					15		
Ala	Met	Trp	Glu	Leu	Val	Tyr	Arg	Thr	Ile	Gly	His	Gln	Leu	His	Trp
			20					25					30		
Ile	Ser	Gly	Tyr	Ile	Ala	Thr	Val	Val	Arg	Gly	Phe	Arg	His	Val	Thr
			35				40						45		
Gln	Gly	Asp	Cys	Lys	His	Tyr	Val	Ile	Leu	Thr	Asn	Thr	Gly	Cys	Ile
			50				55					60			
Cys	Gly	Gly	Gln	Val	Met	Trp	Thr	Val	Pro	Tyr	Cys	Tyr	Pro	Gly	Val
65					70				75						80

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<210> 289
<211> 651
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(651)
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<400> 289																
atg	agg	ggc	acc	cac	atc	ctc	atg	ggg	ctg	agt	ctc	ttc	tat	ccc	atc	48
Met	Arg	Gly	Thr	His	Ile	Leu	Met	Gly	Leu	Ser	Leu	Phe	Tyr	Pro	Ile	
1			5			10			15							
aga	gcc	ctg	gaa	aca	ggg	acc	caa	gtg	gtc	tgc	ggc	cac	cag	ccc	tgg	96
Arg	Ala	Leu	Glu	Thr	Gly	Thr	Gln	Val	Val	Cys	Gly	His	Gln	Pro	Trp	
			20			25			30							
tgt	ggc	ctg	aag	gct	ggg	cgt	cta	ggc	ctc	cgg	cct	cca	ccc	cct	ctg	144
Cys	Gly	Leu	Lys	Ala	Gly	Arg	Leu	Gly	Leu	Arg	Pro	Pro	Pro	Pro	Leu	
35						40						45				
tgc	agt	ggg	cag	tca	cac	ctg	gcg	ggg	ccc	ggc	tgc	ctg	ccc	aga	cag	192
Cys	Ser	Gly	Gln	Ser	His	Leu	Ala	Gly	Pro	Gly	Cys	Leu	Pro	Arg	Gln	
50						55			60							
cag	gtt	ctc	agc	agc	agc	cct	ggc	gtc	cca	gga	gag	ggg	ctt	ctc	tct	240
Gln	Val	Leu	Ser	Ser	Ser	Pro	Gly	Val	Pro	Gly	Glu	Gly	Leu	Leu	Ser	
65			70			75			80							

gct ccc ggc ttc cag gag cac agg gat gcc tgg gtc tgc agc cat gac 288
 Ala Pro Gly Phe Gln Glu His Arg Asp Ala Trp Val Cys Ser His Asp
 85 90 95

ttg ggc agc tgc atc tgt gcc cag agg ggt ggg gct cct gcc tgc tcc 336
 Leu Gly Ser Cys Ile Cys Ala Gln Arg Gly Gly Ala Pro Ala Cys Ser
 100 105 110

atg gag cag aag gcc tgg atc tgc agc tgg gac ttg ggt ggg gct tct 384
 Met Glu Gln Lys Ala Trp Ile Cys Ser Trp Asp Leu Gly Gly Ala Ser
 115 120 125

gcc tgc tct gtg gag cag gag gtc tgg gtc tac agc tgt gac ttc agt 432
 Ala Cys Ser Val Glu Gln Glu Val Trp Val Tyr Ser Cys Asp Phe Ser
 130 135 140

ggc tgc agc tgt gcc cag gag agt ggg gca ccc atc tgc tcc cgg ccc 480
 Gly Cys Ser Cys Ala Gln Glu Ser Gly Ala Pro Ile Cys Ser Arg Pro
 145 150 155 160

gag agc aca ggg atg cct aag tct gca gag agc tac cac cca cct cgg 528
 Glu Ser Thr Gly Met Pro Lys Ser Ala Glu Ser Tyr His Pro Pro Arg
 165 170 175

aag ggg cag ggg ctc tgc ttg tcc gca gct cct gcc agt tcc atg gag 576
 Lys Gly Gln Gly Leu Cys Leu Ser Ala Ala Pro Ala Ser Ser Met Glu
 180 185 190

cat gca gcc ctg gct gtg gct gcc tgc tgc agc tgg cat gat ggc acc 624
 His Ala Ala Leu Ala Val Ala Ala Cys Cys Ser Trp His Asp Gly Thr
 195 200 205

agc cac ttt aga tgg acc cgg gtg taa 651
 Ser His Phe Arg Trp Thr Arg Val *
 210 215

<210> 290

<211> 216

<212> PRT

<213> Homo sapiens

<400> 290

Met Arg Gly Thr His Ile Leu Met Gly Leu Ser Leu Phe Tyr Pro Ile
 1 5 10 15
 Arg Ala Leu Glu Thr Gly Thr Gln Val Val Cys Gly His Gln Pro Trp
 20 25 30
 Cys Gly Leu Lys Ala Gly Arg Leu Gly Leu Arg Pro Pro Pro Leu
 35 40 45
 Cys Ser Gly Gln Ser His Leu Ala Gly Pro Gly Cys Leu Pro Arg Gln
 50 55 60
 Gln Val Leu Ser Ser Ser Pro Gly Val Pro Gly Glu Gly Leu Leu Ser
 65 70 75 80
 Ala Pro Gly Phe Gln Glu His Arg Asp Ala Trp Val Cys Ser His Asp
 85 90 95
 Leu Gly Ser Cys Ile Cys Ala Gln Arg Gly Gly Ala Pro Ala Cys Ser
 100 105 110
 Met Glu Gln Lys Ala Trp Ile Cys Ser Trp Asp Leu Gly Gly Ala Ser
 115 120 125
 Ala Cys Ser Val Glu Gln Glu Val Trp Val Tyr Ser Cys Asp Phe Ser
 130 135 140
 Gly Cys Ser Cys Ala Gln Glu Ser Gly Ala Pro Ile Cys Ser Arg Pro
 145 150 155 160
 Glu Ser Thr Gly Met Pro Lys Ser Ala Glu Ser Tyr His Pro Pro Arg
 165 170 175
 Lys Gly Gln Gly Leu Cys Leu Ser Ala Ala Pro Ala Ser Ser Met Glu
 180 185 190
 His Ala Ala Leu Ala Val Ala Ala Cys Cys Ser Trp His Asp Gly Thr
 195 200 205
 Ser His Phe Arg Trp Thr Arg Val
 210 215

<210> 291

<211> 708

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(708)

<400> 291

atg cgg cct gat gac att aac ccg agg act ggg ctg gtg gtg gcc ctg
 Met Arg Pro Asp Asp Ile Asn Pro Arg Thr Gly Leu Val Val Ala Leu
 1 5 10 15

gtc agt gtc ttc ctc gtc ttt ggt ttc atg ttc acc gtc tct ggg atg Val Ser Val Phe Leu Val Phe Gly Phe Met Phe Thr Val Ser Gly Met 20 25 30	96
aaa ggg gag act ttg gga aac atc ccc ctc ctg gcc atc ggg cca gcc Lys Gly Glu Thr Leu Gly Asn Ile Pro Leu Leu Ala Ile Gly Pro Ala 35 40 45	144
atc tgc cta cca ggc atc gca gcc att gcc ctg gcc agg aaa acc gag Ile Cys Leu Pro Gly Ile Ala Ala Ile Ala Leu Ala Arg Lys Thr Glu 50 55 60	192
gga tgc acc aag tgg cca gag aac gag ctg ctg tgg gtc cgc aaa ttg Gly Cys Thr Lys Trp Pro Glu Asn Glu Leu Leu Trp Val Arg Lys Leu 65 70 75 80	240
ccc tgc ttc cgg aaa ccc aaa gac aag gag gtg gta gag ctg ctg agg Pro Cys Phe Arg Lys Pro Lys Asp Lys Glu Val Val Glu Leu Leu Arg 85 90 95	288
acc cct tca gac cta gaa tcc ggc aag ggg agc tca gat gag ctg gct Thr Pro Ser Asp Leu Glu Ser Gly Lys Gly Ser Ser Asp Glu Leu Ala 100 105 110	336
aag aag gcg ggc ctc agg ggg aag cct ccc cca caa agc cag ggt gag Lys Lys Ala Gly Leu Arg Gly Lys Pro Pro Pro Gln Ser Gln Gly Glu 115 120 125	384
gtg tcc gtg gcc agc tcc atc aac agc ccc aca ccc acg gag gaa gga Val Ser Val Ala Ser Ser Ile Asn Ser Pro Thr Pro Thr Glu Glu Gly 130 135 140	432
gaa tgc cag agc ctc gtc cag aat ggg cat cag gag gag acg tcc aga Glu Cys Gln Ser Leu Val Gln Asn Gly His Gln Glu Glu Thr Ser Arg 145 150 155 160	480
tac ctg gac ggc tac tgc ccc tcg ggc agt tcc ctc acc tac agt gcc Tyr Leu Asp Gly Tyr Cys Pro Ser Gly Ser Ser Leu Thr Tyr Ser Ala 165 170 175	528
ttg gac gtc aag tgc tca gca agg gac aga tct gag tgc cct gag cct Leu Asp Val Lys Cys Ser Ala Arg Asp Arg Ser Glu Cys Pro Glu Pro 180 185 190	576

gag gat agc atc ttc ttt gtg ccc cag gac agt atc atc gtt tgc tcc 624
 Glu Asp Ser Ile Phe Phe Val Pro Gln Asp Ser Ile Ile Val Cys Ser
 195 200 205

 tac aag cag aac agc ccg tat gac aga tac tgt tgt tat atc aat cag 672
 Tyr Lys Gln Asn Ser Pro Tyr Asp Arg Tyr Cys Cys Tyr Ile Asn Gln
 210 215 220

 ata caa ggc agg tgg gac cac gag acc atc gtc taa 708
 Ile Gln Gly Arg Trp Asp His Glu Thr Ile Val *
 225 230 235

<210> 292
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 292
 Met Arg Pro Asp Asp Ile Asn Pro Arg Thr Gly Leu Val Val Ala Leu
 1 5 10 15
 Val Ser Val Phe Leu Val Phe Gly Phe Met Phe Thr Val Ser Gly Met
 20 25 30
 Lys Gly Glu Thr Leu Gly Asn Ile Pro Leu Leu Ala Ile Gly Pro Ala
 35 40 45
 Ile Cys Leu Pro Gly Ile Ala Ala Ile Ala Leu Ala Arg Lys Thr Glu
 50 55 60
 Gly Cys Thr Lys Trp Pro Glu Asn Glu Leu Leu Trp Val Arg Lys Leu
 65 70 75 80
 Pro Cys Phe Arg Lys Pro Lys Asp Lys Glu Val Val Glu Leu Leu Arg
 85 90 95
 Thr Pro Ser Asp Leu Glu Ser Gly Lys Gly Ser Ser Asp Glu Leu Ala
 100 105 110
 Lys Lys Ala Gly Leu Arg Gly Lys Pro Pro Pro Gln Ser Gln Gly Glu
 115 120 125
 Val Ser Val Ala Ser Ser Ile Asn Ser Pro Thr Pro Thr Glu Glu Gly
 130 135 140
 Glu Cys Gln Ser Leu Val Gln Asn Gly His Gln Glu Glu Thr Ser Arg
 145 150 155 160
 Tyr Leu Asp Gly Tyr Cys Pro Ser Gly Ser Ser Leu Thr Tyr Ser Ala
 165 170 175
 Leu Asp Val Lys Cys Ser Ala Arg Asp Arg Ser Glu Cys Pro Glu Pro

180 185 190
 Glu Asp Ser Ile Phe Phe Val Pro Gln Asp Ser Ile Ile Val Cys Ser
 195 200 205
 Tyr Lys Gln Asn Ser Pro Tyr Asp Arg Tyr Cys Cys Tyr Ile Asn Gln
 210 215 220
 Ile Gln Gly Arg Trp Asp His Glu Thr Ile Val
 225 230 235

<210> 293
 <211> 822
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(822)

<400> 293

atg gtg gac ccc acc ggc ttc cgg gag atc gtg gct gcc aat cct ctg 48
 Met Val Asp Pro Thr Gly Phe Arg Glu Ile Val Ala Ala Asn Pro Leu
 1 5 10 15

ctc ctc acg ggc gcc tac atc ctc ctg gcc atg ggg ggc ctg ctc ttt 96
 Leu Leu Thr Gly Ala Tyr Ile Leu Leu Ala Met Gly Gly Leu Leu Phe
 20 25 30

ctg ctc ggc ttc ctg ggc tgc tgc ggg gcc gtc cgt gag aac aag tgt 144
 Leu Leu Gly Phe Leu Gly Cys Cys Gly Ala Val Arg Glu Asn Lys Cys
 35 40 45

ctg ctg cta ttt ctt cct caa ctt cga aaa ggg gaa act aca caa aaa 192
 Leu Leu Leu Phe Leu Pro Gln Leu Arg Lys Gly Glu Thr Thr Gln Lys
 50 55 60

aga gac cgt gag aac agc gtc cgg tgc ccg gcg gtc ccc tgt gag agc 240
 Arg Asp Arg Glu Asn Ser Val Arg Cys Pro Ala Val Pro Cys Glu Ser
 65 70 75 80

aga agc ctg tgt cgg agc cgc tgg agc cca ttc ttc ctg ttc atc ctg 288
 Arg Ser Leu Cys Arg Ser Arg Trp Ser Pro Phe Phe Leu Phe Ile Leu
 85 90 95

atc atc ttc ctg gca gag ctc tca gca gcc atc ctg gcc ttc atc ttc 336

Ile	Ile	Phe	Leu	Ala	Glu	Leu	Ser	Ala	Ala	Ile	Leu	Ala	Phe	Ile	Phe		
			100					105					110				
agg	gaa	aat	gta	cgt	atc	agg	ccc	caa	gct	ttc	ctg	cct	cct	gct	atc	384	
Arg	Glu	Asn	Val	Arg	Ile	Arg	Pro	Gln	Ala	Phe	Leu	Pro	Pro	Ala	Ile		
		115					120					125					
agc	aag	ggg	ttg	gtg	gcc	att	cag	ctc	acc	cga	gaa	ttc	ttc	acc	aag	432	
Ser	Lys	Gly	Leu	Val	Ala	Ile	Gln	Leu	Thr	Arg	Glu	Phe	Phe	Thr	Lys		
		130					135				140						
gag	ctc	acc	aag	cac	tac	cag	ggc	aat	aac	gac	aca	gac	gtc	ttc	tct	480	
Glu	Leu	Thr	Lys	His	Tyr	Gln	Gly	Asn	Asn	Asp	Thr	Asp	Val	Phe	Ser		
		145				150				155					160		
gcc	acc	tgg	aac	tcg	gtc	atg	atc	aca	ttt	ggt	tgc	tgc	ggg	gtc	aac	528	
Ala	Thr	Trp	Asn	Ser	Val	Met	Ile	Thr	Phe	Gly	Cys	Cys	Gly	Val	Asn		
				165					170					175			
ggg	cct	gaa	gac	ttt	aag	ttt	gca	tct	gtg	ttt	cga	ctc	ctg	acc	ctg	576	
Gly	Pro	Glu	Asp	Phe	Lys	Phe	Ala	Ser	Val	Phe	Arg	Leu	Leu	Thr	Leu		
			180					185						190			
gat	agt	gaa	gag	gtg	ccg	gag	gcc	tgc	tgc	cgg	agg	gaa	ccc	caa	agt	624	
Asp	Ser	Glu	Glu	Val	Pro	Glu	Ala	Cys	Cys	Arg	Arg	Glu	Pro	Gln	Ser		
		195					200					205					
cgg	gac	ggg	gtc	ctg	ctg	agc	cgg	gag	gag	tgc	ctc	ctg	gga	agg	agc	672	
Arg	Asp	Gly	Val	Leu	Leu	Ser	Arg	Glu	Glu	Cys	Leu	Leu	Gly	Arg	Ser		
		210				215					220						
cta	ttc	cta	aac	aag	cag	ggc	tgt	tac	acg	gtg	atc	ctc	aac	acc	ttc	720	
Leu	Phe	Leu	Asn	Lys	Gln	Gly	Cys	Tyr	Thr	Val	Ile	Leu	Asn	Thr	Phe		
		225				230				235					240		
gag	acc	tac	gtc	tac	ttg	gcc	gga	gcc	ctt	gcc	atc	ggg	gta	ctg	gcc	768	
Glu	Thr	Tyr	Val	Tyr	Leu	Ala	Gly	Ala	Leu	Ala	Ile	Gly	Val	Leu	Ala		
				245				250						255			
atc	gag	ctt	ttc	gcc	atg	atc	ttt	gcc	atg	tgc	ctc	ttc	cgg	ggc	atc	816	
Ile	Glu	Leu	Phe	Ala	Met	Ile	Phe	Ala	Met	Cys	Leu	Phe	Arg	Gly	Ile		
			260					265					270				

822

<400> 294															
Met 1	Val	Asp	Pro	Thr 5	Gly	Phe	Arg	Glu	Ile 10	Val	Ala	Ala	Asn 15	Pro	Leu
Leu	Leu	Thr	Gly 20	Ala	Tyr	Ile	Leu	Leu 25	Ala	Met	Gly	Gly	Leu 30	Leu	Phe
Leu	Leu	Gly 35	Phe	Leu	Gly	Cys	Cys 40	Gly	Ala	Val	Arg	Glu	Asn 45	Lys	Cys
Leu	Leu	Leu 50	Phe	Leu	Pro	Gln 55	Leu	Arg	Lys	Gly 60	Glu	Thr	Thr	Gln	Lys
Arg 65	Asp	Arg	Glu	Asn 70	Ser	Val	Arg	Cys	Pro	Ala 75	Val	Pro	Cys	Glu	Ser 80
Arg	Ser	Leu	Cys	Arg 85	Ser	Arg	Trp	Ser	Pro 90	Phe	Phe	Leu	Phe	Ile	Leu
Ile	Ile	Phe 100	Leu	Ala	Glu	Leu	Ser	Ala 105	Ala	Ile	Leu	Ala	Phe	Ile	Phe
Arg	Glu	Asn 115	Val	Arg	Ile	Arg	Pro	Gln 120	Ala	Phe	Leu	Pro	Pro	Ala	Ile
Ser	Lys	Gly 130	Leu	Val	Ala	Ile	Gln	Leu 135	Thr	Arg	Glu	Phe	Phe	Thr	Lys
Glu 145	Leu	Thr	Lys	His 150	Tyr	Gln	Gly	Asn	Asn 155	Asp	Thr	Asp	Val	Phe	Ser
Ala	Thr	Trp	Asn	Ser 165	Val	Met	Ile	Thr	Phe 170	Gly	Cys	Cys	Gly	Val	Asn
Gly	Pro	Glu	Asp 180	Phe	Lys	Phe	Ala	Ser	Val 185	Phe	Arg	Leu	Leu	Thr	Leu
Asp	Ser	Glu	Glu 195	Val	Pro	Glu	Ala	Cys	Cys 200	Arg	Arg	Glu	Pro	Gln	Ser
Arg	Asp	Gly 210	Val	Leu	Leu	Ser 215	Arg	Glu	Glu 220	Cys	Leu	Gly	Arg	Ser	
Leu 225	Phe	Leu	Asn	Lys	Gln	Gly	Cys	Tyr	Thr 235	Val	Ile	Leu	Asn	Thr	Phe
Glu	Thr	Tyr	Val 245	Tyr	Leu	Ala	Gly	Ala	Leu 250	Ala	Ile	Gly	Val	Leu	Ala

Ile Glu Leu Phe Ala Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile
 260 265 270
 Gln

<210> 295
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(567)

<400> 295

atg agc aga gac cac agg ctg ctg tgc ctc ctg ggc ctc tgt tgt gtg 48
 Met Ser Arg Asp His Arg Leu Leu Cys Leu Leu Gly Leu Cys Cys Val
 1 5 10 15

gca gat gct tcc aaa cag ccc ttc agg aaa tct gga att ccc aga ggt 96
 Ala Asp Ala Ser Lys Gln Pro Phe Arg Lys Ser Gly Ile Pro Arg Gly
 20 25 30

tat aca ttg cac ctg agg cca tct ggc tac aat cca aac tct ggg tgc 144
 Tyr Thr Leu His Leu Arg Pro Ser Gly Tyr Asn Pro Asn Ser Gly Cys
 35 40 45

ggc tgg cgc caa agc tac tac acc atg ctg cct tct aag ctg cat ttc 192
 Gly Trp Arg Gln Ser Tyr Tyr Thr Met Leu Pro Ser Lys Leu His Phe
 50 55 60

atc tgg aac cgc tgt ggc tgg cag gcc gag cct ctg aac act gca att 240
 Ile Trp Asn Arg Cys Gly Trp Gln Ala Glu Pro Leu Asn Thr Ala Ile
 65 70 75 80

cag gtt aat cat gca gac ctg ctg gag cac gcg ggg ccg agg gga ggc 288
 Gln Val Asn His Ala Asp Leu Leu Glu His Ala Gly Pro Arg Gly Gly
 85 90 95

cca cac tac cgc ttt ccc cac tct ggg gac ggg gag aac ctg att tgt 336
 Pro His Tyr Arg Phe Pro His Ser Gly Asp Gly Glu Asn Leu Ile Cys
 100 105 110

090927.0004
 100927.0004

ctt cgg tcc aca gct agt gtg tgc aag ggc cca att cag gtc cag atc 384
 Leu Arg Ser Thr Ala Ser Val Cys Lys Gly Pro Ile Gln Val Gln Ile
 115 120 125

ggc gtg ctg aca agg act gtg ttt ggg gct gct ccc ctg cag aca gag 432
 Gly Val Leu Thr Arg Thr Val Phe Gly Ala Ala Pro Leu Gln Thr Glu
 130 135 140

ccc cat ggg cag gcc ctg atg ggc ggt cag agg aca caa gac aag agc 480
 Pro His Gly Gln Ala Leu Met Gly Gly Gln Arg Thr Gln Asp Lys Ser
 145 150 155 160

cag ggt gct aag cag acg ccc cta tgg gac atg ggc cag ccg atg ttt 528
 Gln Gly Ala Lys Gln Thr Pro Leu Trp Asp Met Gly Gln Pro Met Phe
 165 170 175

gga tgc ttc caa aca cca aca aca gtt ttg gac gag taa 567
 Gly Cys Phe Gln Thr Pro Thr Thr Val Leu Asp Glu *
 180 185

<210> 296

<211> 188

<212> PRT

<213> Homo sapiens

<400> 296

Met Ser Arg Asp His Arg Leu Leu Cys Leu Leu Gly Leu Cys Cys Val
 1 5 10 15
 Ala Asp Ala Ser Lys Gln Pro Phe Arg Lys Ser Gly Ile Pro Arg Gly
 20 25 30
 Tyr Thr Leu His Leu Arg Pro Ser Gly Tyr Asn Pro Asn Ser Gly Cys
 35 40 45
 Gly Trp Arg Gln Ser Tyr Tyr Thr Met Leu Pro Ser Lys Leu His Phe
 50 55 60
 Ile Trp Asn Arg Cys Gly Trp Gln Ala Glu Pro Leu Asn Thr Ala Ile
 65 70 75 80
 Gln Val Asn His Ala Asp Leu Leu Glu His Ala Gly Pro Arg Gly Gly
 85 90 95
 Pro His Tyr Arg Phe Pro His Ser Gly Asp Gly Glu Asn Leu Ile Cys
 100 105 110
 Leu Arg Ser Thr Ala Ser Val Cys Lys Gly Pro Ile Gln Val Gln Ile
 115 120 125

ctg att gct gtg gtg ggc tcc ctg gcc ttt ctg ctg atg ttc atc gtc 336
 Leu Ile Ala Val Val Gly Ser Leu Ala Phe Leu Leu Met Phe Ile Val
 100 105 110

tgt gcc gcg gtc atc acc cgg cag aag cag aag gcc tcg gcc tat tac 384
 Cys Ala Ala Val Ile Thr Arg Gln Lys Gln Lys Ala Ser Ala Tyr Tyr
 115 120 125

cca tcg tcc ttc ccc aag aag aag tac gtg gac cag agt gac cgg gcc 432
 Pro Ser Ser Phe Pro Lys Lys Lys Tyr Val Asp Gln Ser Asp Arg Ala
 130 135 140

ggg ggc ccc cgg gcc ttc agt gag gtc ccc gac aga gcc ccc gac agc 480
 Gly Gly Pro Arg Ala Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser
 145 150 155 160

agg ccc gag gaa gcc ctg gat tcc tcc cgg cag ctc cag gcc gac atc 528
 Arg Pro Glu Glu Ala Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile
 165 170 175

ttg gcc gcc acc cag aac ctc aag tcc ccc acc agg gct gca ctg ggc 576
 Leu Ala Ala Thr Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly
 180 185 190

ggt ggg gac gga gcc agg atg gtg gag ggc agg ggc gca gag gaa gag 624
 Gly Gly Asp Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu
 195 200 205

gag aag ggc agc cag gag ggg gac cag gaa gtc cag gga cat ggg gtc 672
 Glu Lys Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val
 210 215 220

cca gtg gag aca cca gag gcg cag gag gag ccg tgc tca ggg gtc ctt 720
 Pro Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 225 230 235 240

gag ggg gct gtg gtg gcc ggt gag ggc caa ggg gag ctg gaa ggg tct 768
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly Ser
 245 250 255

ctc ttg tta gcc cag gaa gcc cag gga cca gtg ggt ccc ccc gaa agc 816
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270

852

<400> 298

Met 1	Val	Ser	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	Leu	15
Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	Lys	Ala
			20					25					30		
Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser
		35					40					45			
Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	Ala	Leu	Ser	Pro
	50					55					60				
Thr	Ser	Met	Gly	Pro	Gln	Pro	Ile	Thr	Leu	Gly	Gly	Pro	Ser	Pro	Pro
65					70					75					80
Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr	Val	Met
				85				90						95	
Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	Phe	Leu	Leu	Met	Phe	Ile	Val
			100					105					110		
Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr
		115					120					125			
Pro	Ser	Ser	Phe	Pro	Lys	Lys	Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala
	130					135					140				
Gly	Gly	Pro	Arg	Ala	Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser
145					150					155					160
Arg	Pro	Glu	Glu	Ala	Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile
				165					170					175	
Leu	Ala	Ala	Thr	Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly
			180					185					190		
Gly	Gly	Asp	Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu
		195					200					205			
Glu	Lys	Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val
	210					215					220				
Pro	Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
225					230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	Ser

245 250 255
 Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro Glu Ser
 260 265 270
 Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
 275 280

<210> 299
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(369)

<400> 299
 atg gcc ctg ggc aag gtt ctg gcc atg gca ctg gtt ttg gcc ttg gcc 48
 Met Ala Leu Gly Lys Val Leu Ala Met Ala Leu Val Leu Ala Leu Ala
 1 5 10 15
 gtg ctg ggg tcg ctg tcc cct ggg gcc cgg gcg ggg gac tgc aag ggg 96
 Val Leu Gly Ser Leu Ser Pro Gly Ala Arg Ala Gly Asp Cys Lys Gly
 20 25 30
 cag cgg cag gtg ctg cgg gag gcg cca ggc ttc gtg acg gat ggt gcg 144
 Gln Arg Gln Val Leu Arg Glu Ala Pro Gly Phe Val Thr Asp Gly Ala
 35 40 45
 ggc aac tac agc gtc aat ggc aac tgc gag tgg ctc atc gag gaa ccc 192
 Gly Asn Tyr Ser Val Asn Gly Asn Cys Glu Trp Leu Ile Glu Glu Pro
 50 55 60
 tgc ccc agt ggc tct ttc tct gtg aag aca tgt ggc tta acc tgg ggt 240
 Cys Pro Ser Gly Ser Phe Ser Val Lys Thr Cys Gly Leu Thr Trp Gly
 65 70 75 80
 ata gct gag atc aga ggc atc tgt acg agg gag cag aag ggc att cca 288
 Ile Ala Glu Ile Arg Gly Ile Cys Thr Arg Glu Gln Lys Gly Ile Pro
 85 90 95
 ggc aag aat agc tgt gca aag gcg ggg aag cgg gag agt gat gct ttt 336
 Gly Lys Asn Ser Cys Ala Lys Ala Gly Lys Arg Glu Ser Asp Ala Phe
 100 105 110

gaa gaa cta gaa atc cag tgt gtt aaa aca tag
 Glu Glu Leu Glu Ile Gln Cys Val Lys Thr *
 115 120

369

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 300
 Met Ala Leu Gly Lys Val Leu Ala Met Ala Leu Val Leu Ala Leu Ala
 1 5 10 15
 Val Leu Gly Ser Leu Ser Pro Gly Ala Arg Ala Gly Asp Cys Lys Gly
 20 25 30
 Gln Arg Gln Val Leu Arg Glu Ala Pro Gly Phe Val Thr Asp Gly Ala
 35 40 45
 Gly Asn Tyr Ser Val Asn Gly Asn Cys Glu Trp Leu Ile Glu Glu Pro
 50 55 60
 Cys Pro Ser Gly Ser Phe Ser Val Lys Thr Cys Gly Leu Thr Trp Gly
 65 70 75 80
 Ile Ala Glu Ile Arg Gly Ile Cys Thr Arg Glu Gln Lys Gly Ile Pro
 85 90 95
 Gly Lys Asn Ser Cys Ala Lys Ala Gly Lys Arg Glu Ser Asp Ala Phe
 100 105 110
 Glu Glu Leu Glu Ile Gln Cys Val Lys Thr
 115 120

<210> 301
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(411)

<400> 301
 atg gac gca tac agc gcg tct tta agc ggt ccc aac agc ctc ggg ctg
 Met Asp Ala Tyr Ser Ala Ser Leu Ser Gly Pro Asn Ser Leu Gly Leu
 1 5 10 15

48

<400> 302
Met Asp Ala Tyr Ser Ala Ser Leu Ser Gly Pro Asn Ser Leu Gly Leu
1 5 10 15
Ser Thr Leu Val Pro Pro Ser Asn Ala Arg Glu Cys Pro Thr Glu Pro
20 25 30

Pro Lys Ile Leu Ser Leu Ser Val Pro Pro Ser Pro Ala Val Glu Pro
 35 40 45
 Arg Pro Arg Trp Lys Glu Asn Lys Thr Lys Ser Gly Ser Arg Gly Ser
 50 55 60
 Ser Ser Ala Asp Asn Cys Gln Gly Ser Asn Glu Leu Asn Gly Phe Pro
 65 70 75 80
 Glu Ala Ala Ile Thr Lys Thr Thr Lys Leu Val Ser Gln Gln Met Tyr
 85 90 95
 Ile Glu Cys Leu Leu His Thr Arg His Cys Cys Arg Pro Arg Glu Tyr
 100 105 110
 Ser Cys Glu Gln Asn Ser Glu Asp Thr Ser Ser Glu Thr Val Cys Gly
 115 120 125
 Asp Glu Asn Ala Pro Gln Glu Leu
 130 135

<210> 303

<211> 915

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(915)

<400> 303

atg ctg ccg ccg ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc 48
 Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu
 1 5 10 15

ctg cta ctg ctg gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca 96
 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro
 20 25 30

tcc cca ggc cca gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg 144
 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
 35 40 45

gag ggc gag ggc tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg 192
 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
 50 55 60

cgg ggc tgc ctg gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg 240
 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp


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      130              135              140
Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
145              150              155              160
Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
      165              170              175
His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
      180              185              190
Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
      195              200              205
Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
      210              215              220
Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
225              230              235              240
Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Arg
      245              250              255
Asn Ala Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr
      260              265              270
Pro Asp Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn
      275              280              285
Leu Val Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
      290              295              300

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<210> 305
<211> 645
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(645)

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<400> 305
atg ctg aat gtc tcc ggc ctc ttt gtt ctc ctc tgt ggg ctg ctt gtc      48
Met Leu Asn Val Ser Gly Leu Phe Val Leu Leu Cys Gly Leu Leu Val
  1              5              10              15

tca tcc tct gca cag gag gtc ctg gct gga gtt tct tcc cag ctc ctt      96
Ser Ser Ser Ala Gln Glu Val Leu Ala Gly Val Ser Ser Gln Leu Leu
      20              25              30

aat gat ttg act caa gga ctc ctc agg gca gac ttt ctt ccc agc ctg      144
Asn Asp Leu Thr Gln Gly Leu Leu Arg Ala Asp Phe Leu Pro Ser Leu
      35              40              45

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gac gcc gac tcc ccc gtt tga 645
Asp Ala Asp Ser Pro Val *

210

<210> 306
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 306

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Met Leu Asn Val Ser Gly Leu Phe Val Leu Leu Cys Gly Leu Leu Val
 1          5          10          15
Ser Ser Ser Ala Gln Glu Val Leu Ala Gly Val Ser Ser Gln Leu Leu
 20          25          30
Asn Asp Leu Thr Gln Gly Leu Leu Arg Ala Asp Phe Leu Pro Ser Leu
 35          40          45
Gln Thr Thr Gly Leu Gln Lys Pro Leu Ser Ser Ala Phe Asp Gly Val
 50          55          60
Ser Gly Leu Leu Asp Ile Phe Gly Pro Pro Leu Thr Asn Glu Ile Asn
 65          70          75          80
Thr Val Ser Ile Gln Val Lys Asn Pro Gln Leu Leu His Val Ser Ile
 85          90          95
Glu Ser Thr Pro Gln Arg Lys Glu Ala Thr Val Gln Val Pro Phe Thr
100          105          110
Ser Glu Leu Ile Val Gln Leu Leu Thr Met Lys Pro Phe Thr Ala Asn
115          120          125
Met Gln Ser Asp Ile Lys Val Gln Ile Arg Leu Glu Lys Asn Val Gly
130          135          140
Gly Arg Tyr Glu Leu Ala Phe Gly Asn Cys Arg Leu Leu Pro Glu Ala
145          150          155          160
Ile Trp Ile Gln Thr Gly Val His Glu Lys Thr Gln Gly Ala Ile Ser
165          170          175
Ile Arg Arg Ala Ile Pro Arg Ile Val Gln Pro Thr Val Ser His Gln
180          185          190
Gln Arg Leu Gly Gly Arg Ala Arg Gln His Ser Ala Gln Arg Lys Phe
195          200          205
Asp Ala Asp Ser Pro Val
210

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<210> 307
 <211> 480
 <212> DNA
 <213> Homo sapiens

F00290-22650

<220>

<221> CDS

<222> (1)...(480)

<400> 307

atg	agc	caa	gtg	tta	gcg	agc	ctt	gct	ctg	agc	agt	cgt	acg	gca	cag	48
Met	Ser	Gln	Val	Leu	Ala	Ser	Leu	Ala	Leu	Ser	Ser	Arg	Thr	Ala	Gln	
1				5				10						15		

gcg	cga	aca	ttg	aac	ctg	acg	aag	agc	aga	ttt	aaa	gga	ctc	gcc	gtc	96
Ala	Arg	Thr	Leu	Asn	Leu	Thr	Lys	Ser	Arg	Phe	Lys	Gly	Leu	Ala	Val	
			20				25						30			

cct	tgg	atg	gag	aaa	acc	act	gtt	gca	cag	gta	aga	acg	gca	tat	agc	144
Pro	Trp	Met	Glu	Lys	Thr	Thr	Val	Ala	Gln	Val	Arg	Thr	Ala	Tyr	Ser	
		35					40					45				

tgg	cac	gtg	cac	tac	cac	agc	ctc	tgc	ctc	gag	tgg	cca	tgg	cag	aca	192
Trp	His	Val	His	Tyr	His	Ser	Leu	Cys	Leu	Glu	Trp	Pro	Trp	Gln	Thr	
	50					55				60						

ctg	cca	ttc	aat	cct	ggt	ctg	aac	aca	acc	ccc	ttc	cca	aca	cag	ctg	240
Leu	Pro	Phe	Asn	Pro	Gly	Leu	Asn	Thr	Thr	Pro	Phe	Pro	Thr	Gln	Leu	
65					70				75					80		

tct	aca	tcc	tac	ccg	tca	gag	cag	gca	cac	cat	gtg	aaa	ctt	ctc	tgc	288
Ser	Thr	Ser	Tyr	Pro	Ser	Glu	Gln	Ala	His	His	Val	Lys	Leu	Leu	Cys	
				85				90						95		

cat	tcc	ttg	cct	agt	ggc	tct	gta	cac	agt	gtt	cct	aag	ctc	ctc	tat	336
His	Ser	Leu	Pro	Ser	Gly	Ser	Val	His	Ser	Val	Pro	Lys	Leu	Leu	Tyr	
			100				105						110			

tgg	gct	ccc	acg	gga	ctc	tat	att	cga	gac	cac	att	cca	cct	gcc	cta	384
Trp	Ala	Pro	Thr	Gly	Leu	Tyr	Ile	Arg	Asp	His	Ile	Pro	Pro	Ala	Leu	
		115				120						125				

atc	acc	ccg	ggg	cct	agt	acc	cgg	caa	cta	gga	aca	gcc	cca	gca	ccc	432
Ile	Thr	Pro	Gly	Pro	Ser	Thr	Arg	Gln	Leu	Gly	Thr	Ala	Pro	Ala	Pro	
	130					135				140						

ctg	aac	cca	cta	caa	tta	ttc	aaa	cta	gcc	agt	gct	aaa	cct	gct	taa	480
Leu	Asn	Pro	Leu	Gln	Leu	Phe	Lys	Leu	Ala	Ser	Ala	Lys	Pro	Ala	*	

145

150

155

<210> 308

<211> 159

<212> PRT

<213> Homo sapiens

<400> 308

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Met Ser Gln Val Leu Ala Ser Leu Ala Leu Ser Ser Arg Thr Ala Gln
 1          5          10          15
Ala Arg Thr Leu Asn Leu Thr Lys Ser Arg Phe Lys Gly Leu Ala Val
          20          25          30
Pro Trp Met Glu Lys Thr Thr Val Ala Gln Val Arg Thr Ala Tyr Ser
          35          40          45
Trp His Val His Tyr His Ser Leu Cys Leu Glu Trp Pro Trp Gln Thr
          50          55          60
Leu Pro Phe Asn Pro Gly Leu Asn Thr Thr Pro Phe Pro Thr Gln Leu
65          70          75          80
Ser Thr Ser Tyr Pro Ser Glu Gln Ala His His Val Lys Leu Leu Cys
          85          90          95
His Ser Leu Pro Ser Gly Ser Val His Ser Val Pro Lys Leu Leu Tyr
          100         105         110
Trp Ala Pro Thr Gly Leu Tyr Ile Arg Asp His Ile Pro Pro Ala Leu
          115         120         125
Ile Thr Pro Gly Pro Ser Thr Arg Gln Leu Gly Thr Ala Pro Ala Pro
          130         135         140
Leu Asn Pro Leu Gln Leu Phe Lys Leu Ala Ser Ala Lys Pro Ala
145          150          155

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<210> 309

<211> 907

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(907)

<400> 309

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atg ctg ttc ctc gtc ctc ctg ctg ccc ctg gag ctg agc ctg gca ggc
Met Leu Phe Leu Val Leu Leu Leu Pro Leu Glu Leu Ser Leu Ala Gly
 1          5          10          15

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180	185	190	
tcc ctg atc ctg ccc gtc acc	tcc ctg cgg ccc cag cag	gca cag ccc	624
Ser Leu Ile Leu Pro Val Thr	Ser Leu Arg Pro Gln Gln	Ala Gln Pro	
195	200	205	
agg tct gac ggg gag gtg atg	ccc acg ctg gac atg gcc	ttg ttc gac	672
Arg Ser Asp Gly Glu Val Met	Pro Thr Leu Asp Met Ala	Leu Phe Asp	
210	215	220	
tgg acc gat tat gaa gac tta	aaa cct gat ggt tgg ccc	tct gca aag	720
Trp Thr Asp Tyr Glu Asp Leu	Lys Pro Asp Gly Trp Pro	Ser Ala Lys	
225	230	235	240
aag aaa gag aaa cac cgc ggt	aaa ctc tcc agt gat ggt	aac gaa aca	768
Lys Lys Glu Lys His Arg Gly	Lys Leu Ser Ser Asp Gly	Asn Glu Thr	
245	250	255	
tca cca gcc gaa ggg gaa cca	tgc gac cat cac caa gac	tgc ctg cca	816
Ser Pro Ala Glu Gly Glu Pro	Cys Asp His His Gln Asp	Cys Leu Pro	
260	265	270	
ggg act tgc tgc gac ctg cgg	gag cat ctc tgc aca ccc	cac aac cga	864
Gly Thr Cys Cys Asp Leu Arg	Glu His Leu Cys Thr Pro	His Asn Arg	
275	280	285	
ggc ctc aac aac aaa tgc ttc	gat gac tgc atg tgt gtg	gaa g	907
Gly Leu Asn Asn Lys Cys Phe	Asp Asp Cys Met Cys Val	Glu	
290	295	300	

<210> 310

<211> 302

<212> PRT

<213> Homo sapiens

<400> 310

Met Leu Phe Leu Val Leu Leu Leu Pro Leu Glu Leu Ser Leu Ala Gly	
1 5 10 15	
Ala Leu Ala Pro Gly Thr Pro Ala Arg Asn Leu Pro Glu Asn His Ile	
20 25 30	
Asp Leu Pro Gly Pro Ala Leu Trp Thr Pro Gln Ala Ser His His Arg	
35 40 45	

Arg Arg Gly Pro Gly Lys Lys Glu Trp Gly Pro Gly Leu Pro Ser Gln
 50 55 60
 Ala Gln Asp Gly Ala Val Val Thr Ala Thr Arg Gln Ala Ser Arg Leu
 65 70 75 80
 Pro Glu Ala Glu Gly Leu Leu Pro Glu Gln Ser Pro Ala Gly Leu Leu
 85 90 95
 Gln Asp Lys Asp Leu Leu Leu Gly Leu Ala Leu Pro Tyr Pro Glu Lys
 100 105 110
 Glu Asn Arg Pro Pro Gly Trp Glu Arg Thr Arg Lys Arg Ser Arg Glu
 115 120 125
 His Lys Arg Arg Arg Asp Arg Leu Arg Leu His Gln Gly Arg Ala Leu
 130 135 140
 Val Arg Gly Pro Ser Ser Leu Met Lys Lys Ala Glu Leu Ser Glu Ala
 145 150 155 160
 Gln Val Leu Asp Ala Ala Met Glu Glu Ser Ser Thr Ser Leu Ala Pro
 165 170 175
 Thr Met Phe Phe Leu Thr Thr Phe Glu Ala Ala Pro Ala Thr Glu Glu
 180 185 190
 Ser Leu Ile Leu Pro Val Thr Ser Leu Arg Pro Gln Gln Ala Gln Pro
 195 200 205
 Arg Ser Asp Gly Glu Val Met Pro Thr Leu Asp Met Ala Leu Phe Asp
 210 215 220
 Trp Thr Asp Tyr Glu Asp Leu Lys Pro Asp Gly Trp Pro Ser Ala Lys
 225 230 235 240
 Lys Lys Glu Lys His Arg Gly Lys Leu Ser Ser Asp Gly Asn Glu Thr
 245 250 255
 Ser Pro Ala Glu Gly Glu Pro Cys Asp His His Gln Asp Cys Leu Pro
 260 265 270
 Gly Thr Cys Cys Asp Leu Arg Glu His Leu Cys Thr Pro His Asn Arg
 275 280 285
 Gly Leu Asn Asn Lys Cys Phe Asp Asp Cys Met Cys Val Glu
 290 295 300

<210> 311
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(670)

<400> 311

ggc gtc aga ctc cag gat ctt gga ctt ttg gaa tct tgg att tac acc 384
 Gly Val Arg Leu Gln Asp Leu Gly Leu Leu Glu Ser Trp Ile Tyr Thr
 115 120 125

agt ggt cta cct gag gct ctt ggg cct ccg gcc ata gag tga 426
 Ser Gly Leu Pro Glu Ala Leu Gly Pro Pro Ala Ile Glu *
 130 135 140

<210> 314

<211> 141

<212> PRT

<213> Homo sapiens

<400> 314

Met Glu Gly Asp Pro Gly Gly Leu Leu Leu Leu Leu Ala Gly Val
 1 5 10 15
 Gly Gly Tyr Gln Leu Gly Thr Arg Arg Asn Phe Ser His Gly Glu Lys
 20 25 30
 Val Asn Asp Lys Ile Pro Val Ala Thr Ile Ser Ile Trp Asp Lys Tyr
 35 40 45
 Ser Pro His His Trp Gly Pro Leu Gln Ser Ser Gln Ala Leu Ser Pro
 50 55 60
 Pro Glu Gly Ala Asn Trp Ser Pro His Ser Cys Ala Val Ser Thr Lys
 65 70 75 80
 Gly Ala Asp Thr Val His Cys Pro Arg Trp Ser Thr Gln Leu Leu Tyr
 85 90 95
 Cys Thr Ile Leu Glu Leu Gly Leu Pro Leu Glu Cys Ala Leu Leu Gln
 100 105 110
 Gly Val Arg Leu Gln Asp Leu Gly Leu Leu Glu Ser Trp Ile Tyr Thr
 115 120 125
 Ser Gly Leu Pro Glu Ala Leu Gly Pro Pro Ala Ile Glu
 130 135 140

<210> 315

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(375)

<400> 315

atg	gtc	ctg	tgc	tgg	ctg	ctg	ctt	ctg	gtg	atg	gct	ctg	ccc	cca	ggc	48
Met	Val	Leu	Cys	Trp	Leu	Leu	Leu	Leu	Val	Met	Ala	Leu	Pro	Pro	Gly	
1				5					10					15		

acg	acg	ggc	gtc	aag	gac	tgc	gtc	ttc	tgt	gag	ctc	acc	gac	tcc	atg	96
Thr	Thr	Gly	Val	Lys	Asp	Cys	Val	Phe	Cys	Glu	Leu	Thr	Asp	Ser	Met	
		20						25					30			

cag	tgt	cct	ggt	acc	tac	atg	cac	tgt	ggc	gat	gac	gag	gac	tgc	ttc	144
Gln	Cys	Pro	Gly	Thr	Tyr	Met	His	Cys	Gly	Asp	Asp	Glu	Asp	Cys	Phe	
		35					40					45				

aca	ggc	cac	ggg	gtc	gcc	ccg	ggc	act	ggt	ccg	gtc	atc	aac	aaa	ggc	192
Thr	Gly	His	Gly	Val	Ala	Pro	Gly	Thr	Gly	Pro	Val	Ile	Asn	Lys	Gly	
	50					55					60					

tgc	ctg	cga	gcc	acc	agc	tgc	ggc	ctt	gag	gaa	ccc	gtc	agc	tac	agg	240
Cys	Leu	Arg	Ala	Thr	Ser	Cys	Gly	Leu	Glu	Glu	Pro	Val	Ser	Tyr	Arg	
65					70				75					80		

ggc	gtc	acc	tac	agc	ctc	acc	acc	aac	tgc	tgc	acc	ggc	cgc	ctg	tgt	288
Gly	Val	Thr	Tyr	Ser	Leu	Thr	Thr	Asn	Cys	Cys	Thr	Gly	Arg	Leu	Cys	
				85				90						95		

aac	aga	gcc	ccg	agc	agc	cag	aca	gtg	ggg	gcc	acc	acc	agc	ctg	gca	336
Asn	Arg	Ala	Pro	Ser	Ser	Gln	Thr	Val	Gly	Ala	Thr	Thr	Ser	Leu	Ala	
		100					105						110			

ctg	ggg	ctg	ggt	atg	ctg	ctt	cct	cca	cgt	ttg	ctg	tga				375
Leu	Gly	Leu	Gly	Met	Leu	Leu	Pro	Pro	Arg	Leu	Leu	*				
	115						120									

<210> 316

<211> 124

<212> PRT

<213> Homo sapiens

<400> 316

Met	Val	Leu	Cys	Trp	Leu	Leu	Leu	Leu	Val	Met	Ala	Leu	Pro	Pro	Gly	
1				5					10					15		

Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 20 25 30
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 35 40 45
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 50 55 60
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 65 70 75 80
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 85 90 95
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 100 105 110
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
 115 120

<210> 317
 <211> 688
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(688)

<400> 317

atg gag ccc ctg cgc gcg ccc gcg ctg cgc cgc ctg ctg ccg ccg ctg 48
 Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu
 1 5 10 15

ctg ctc ctg ctg ctg tca ctg ccc ccc cgc gcc cgg gcc aag tac gtg 96
 Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
 20 25 30

cgg ggc aac ctc agt tcc aag gag gac tgg gtg ttc ctg aca aga ttt 144
 Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
 35 40 45

tgt ttc ctc tcg gat tac ggc cga ctg gac ttc cgt ttc cgc tac cct 192
 Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
 50 55 60

gag gcc aag tgc tgt cag aac atc ctc ctc tat ttt gat gac cca tcc 240
 Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser

<210> 318
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 318

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Met Glu Pro Leu Arg Ala Pro Ala Leu Arg Arg Leu Leu Pro Pro Leu
 1          5          10          15
Leu Leu Leu Leu Leu Ser Leu Pro Pro Arg Ala Arg Ala Lys Tyr Val
 20          25          30
Arg Gly Asn Leu Ser Ser Lys Glu Asp Trp Val Phe Leu Thr Arg Phe
 35          40          45
Cys Phe Leu Ser Asp Tyr Gly Arg Leu Asp Phe Arg Phe Arg Tyr Pro
 50          55          60
Glu Ala Lys Cys Cys Gln Asn Ile Leu Leu Tyr Phe Asp Asp Pro Ser
 65          70          75          80
Gln Trp Pro Ala Val Tyr Lys Ala Gly Asp Lys Asp Cys Leu Ala Lys
 85          90          95
Glu Ser Val Ile Arg Pro Glu Asn Asn Gln Val Ile Asn Leu Thr Thr
 100         105         110
Gln Tyr Ala Trp Ser Gly Cys Gln Val Val Ser Glu Glu Gly Thr Arg
 115         120         125
Tyr Leu Ser Cys Ser Ser Gly Arg Ser Phe Arg Ser Val Arg Glu Arg
 130         135         140
Trp Trp Tyr Ile Ala Leu Ser Lys Cys Gly Gly Asp Gly Leu Gln Leu
 145         150         155         160
Glu Tyr Glu Met Val Leu Thr Asn Gly Lys Ser Phe Trp Thr Arg His
 165         170         175
Phe Ser Ala Asp Glu Phe Gly Ile Leu Glu Thr Asp Val Thr Phe Leu
 180         185         190
Leu Ile Phe Ile Leu Ile Phe Phe Leu Ser Cys Tyr Phe Gly Tyr Leu
 195         200         205
Leu Lys Gly Arg Gln Leu Leu His Thr Thr Tyr Lys Met Phe Met Ala
 210         215         220
Ala Ala Gly Val Glu
225

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<210> 319
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(765)

<400> 319

atg gga gct cca aag ctg gcc aag ctg cac aca gcc ctg ctg gcg tcc	48
Met Gly Ala Pro Lys Leu Ala Lys Leu His Thr Ala Leu Leu Ala Ser	
1 5 10 15	

agc ctg gct cta ggc cag gag cct tgg ctg gag ggc ggc cca gcg ccc	96
Ser Leu Ala Leu Gly Gln Glu Pro Trp Leu Glu Gly Gly Pro Ala Pro	
20 25 30	

cga cag cca cgt cca gca cct tca gca ggt tct ccc cgg cag cac ttg	144
Arg Gln Pro Arg Pro Ala Pro Ser Ala Gly Ser Pro Arg Gln His Leu	
35 40 45	

gca gtc aga tgt ggc cag acg gtc cct tcc aga gag agc tgt cgt ggc	192
Ala Val Arg Cys Gly Gln Thr Val Pro Ser Arg Glu Ser Cys Arg Gly	
50 55 60	

ccc aaa ggc atg aac gtg gcc ctc cgt gca cgg caa gca gta cag gaa	240
Pro Lys Gly Met Asn Val Ala Leu Arg Ala Arg Gln Ala Val Gln Glu	
65 70 75 80	

cgt gtt cgg aag gca gag tgc gcg gcc aac agc tgt gct gcc ctg gac	288
Arg Val Arg Lys Ala Glu Cys Ala Ala Asn Ser Cys Ala Ala Leu Asp	
85 90 95	

aag tgc cct cca cct caa cag ttt ccc ctg caa ggc ctc cat gat gag	336
Lys Cys Pro Pro Pro Gln Gln Phe Pro Leu Gln Gly Leu His Asp Glu	
100 105 110	

cgg aac aca gcc act cct ggg gaa ggg cac aag cag cag tca cac gtc	384
Arg Asn Thr Ala Thr Pro Gly Glu Gly His Lys Gln Gln Ser His Val	
115 120 125	

gca ctg aag tgg ctg gat gga cgc cag aga gtc cag agg cag aca gga	432
Ala Leu Lys Trp Leu Asp Gly Arg Gln Arg Val Gln Arg Gln Thr Gly	
130 135 140	

aac aca aaa tgg aag atg ctg gtg cac gca gaa agt ctt gga gga gga	480
Asn Thr Lys Trp Lys Met Leu Val His Ala Glu Ser Leu Gly Gly Gly	
145 150 155 160	

gag cca gaa acc ttc aca aaa tcc aaa tca gac ctc gtc tct gct cac 528
 Glu Pro Glu Thr Phe Thr Lys Ser Lys Ser Asp Leu Val Ser Ala His
 165 170 175

ttc acc ccg tcg cag ctt ctt acg ctc ccc ccc att ttt aca gac aag 576
 Phe Thr Pro Ser Gln Leu Leu Thr Leu Pro Pro Ile Phe Thr Asp Lys
 180 185 190

gaa act gag tcc cag agg ccc gga aat ggg gag ggc ggg gag tca gga 624
 Glu Thr Glu Ser Gln Arg Pro Gly Asn Gly Glu Gly Gly Glu Ser Gly
 195 200 205

cag gtg gca gga aca ggg ctg cct cta ggg caa ctg atg aac cct ggc 672
 Gln Val Ala Gly Thr Gly Leu Pro Leu Gly Gln Leu Met Asn Pro Gly
 210 215 220

agc agc atc cgt gac act gga gag ccc aac acc agc tgc cac tgt gtg 720
 Ser Ser Ile Arg Asp Thr Gly Glu Pro Asn Thr Ser Cys His Cys Val
 225 230 235 240

gcc ctg tgg cat tgg cca caa atg agc aca tcc atc agc tcc tga 765
 Ala Leu Trp His Trp Pro Gln Met Ser Thr Ser Ile Ser Ser *
 245 250

<210> 320

<211> 254

<212> PRT

<213> Homo sapiens

<400> 320

Met Gly Ala Pro Lys Leu Ala Lys Leu His Thr Ala Leu Leu Ala Ser
 1 5 10 15
 Ser Leu Ala Leu Gly Gln Glu Pro Trp Leu Glu Gly Gly Pro Ala Pro
 20 25 30
 Arg Gln Pro Arg Pro Ala Pro Ser Ala Gly Ser Pro Arg Gln His Leu
 35 40 45
 Ala Val Arg Cys Gly Gln Thr Val Pro Ser Arg Glu Ser Cys Arg Gly
 50 55 60
 Pro Lys Gly Met Asn Val Ala Leu Arg Ala Arg Gln Ala Val Gln Glu
 65 70 75 80
 Arg Val Arg Lys Ala Glu Cys Ala Ala Asn Ser Cys Ala Ala Leu Asp

```

<210> 321
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(339)

<400> 321
atg gtg ctc acc aat acg gct tct ttc tat gca gct ctg cag cta ctg      48
Met Val Leu Thr Asn Thr Ala Ser Phe Tyr Ala Ala Leu Gln Leu Leu
  1                      5                      10                      15

ctg gct ctt ctg gga att ttt tct ttt gta tat ccg tcc ctg gtg gat      96
Leu Ala Leu Leu Gly Ile Phe Ser Phe Val Tyr Pro Ser Leu Val Asp
                20                      25                      30

cac ttg ccc ttt cct gcc aaa ccc ttg cct ctg tct gaa ttc tgg ttt      144
His Leu Pro Phe Pro Ala Lys Pro Leu Pro Leu Ser Glu Phe Trp Phe
      35                      40                      45

```

ttt gca gca ata gga aaa agg tcc ccc ttc ttc agg gca ccc atg atc 240
Phe Ala Ala Ile Gly Lys Arg Ser Pro Phe Phe Arg Ala Pro Met Ile
65 70 75 80

ttg aaa cag aga ctc atg aag act cat gaa tgg gtt tca act ccc atc 288
Leu Lys Gln Arg Leu Met Lys Thr His Glu Trp Val Ser Thr Pro Ile
85 90 95

cat cct ctc tgc caa gcc ctt gtg gag acc aca gtc cat gac cct gaa 336
His Pro Leu Cys Gln Ala Leu Val Glu Thr Thr Val His Asp Pro Glu
100 105 110

taa	339
*	

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<210> 322
<211> 112
<212> PRT
<213> Homo sapiens
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<400> 322

Met	Val	Leu	Thr	Asn	Thr	Ala	Ser	Phe	Tyr	Ala	Ala	Leu	Gln	Leu	Leu
1				5					10					15	
Leu	Ala	Leu	Leu	Gly	Ile	Phe	Ser	Phe	Val	Tyr	Pro	Ser	Leu	Val	Asp
			20					25					30		
His	Leu	Pro	Phe	Pro	Ala	Lys	Pro	Leu	Pro	Leu	Ser	Glu	Phe	Trp	Phe
		35					40					45			
Gly	Ser	Ser	Phe	Val	Ala	Pro	Arg	Ala	Ser	Ala	Asn	Leu	Val	Gly	Ala
	50					55					60				
Phe	Ala	Ala	Ile	Gly	Lys	Arg	Ser	Pro	Phe	Phe	Arg	Ala	Pro	Met	Ile
65					70					75					80
Leu	Lys	Gln	Arg	Leu	Met	Lys	Thr	His	Glu	Trp	Val	Ser	Thr	Pro	Ile
				85					90					95	
His	Pro	Leu	Cys	Gln	Ala	Leu	Val	Glu	Thr	Thr	Val	His	Asp	Pro	Glu
			100					105					110		

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<220>
<221> CDS
<222> (1)...(888)
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atg cgc ctc cac ctg ctc ctg ctg ctc gcg ctg tgc ggt gca ggc acc 48
Met Arg Leu His Leu Leu Leu Leu Leu Ala Leu Cys Gly Ala Gly Thr
1 5 10 15

acc gcc gcg gag ctc agt tac agc ttg cgt ggc aac tgg agc atc tgc 96
Thr Ala Ala Glu Leu Ser Tyr Ser Leu Arg Gly Asn Trp Ser Ile Cys
20 25 30

aat ggg aac ggc tcg ctg gag ctg ccc ggg gcg gtc cct ggc tgc gtg 144
Asn Gly Asn Gly Ser Leu Glu Leu Pro Gly Ala Val Pro Gly Cys Val
35 40 45

cac agc gcc ttg ttc cag cag ggc ctg atc cag gtc act ctg ttg tgt 192
 His Ser Ala Leu Phe Gln Gln Gly Leu Ile Gln Val Thr Leu Leu Cys
 50 55 60

gaa ggc tac agt gca gga gag tgg aag cct gga gac caa cca ggg gac 240
Glu Gly Tyr Ser Ala Gly Glu Trp Lys Pro Gly Asp Gln Pro Gly Asp
65 70 75 80

tat tgc tgg tct atg tat ggg caa gag atg act tct ggc ttg gac aag 288
Tyr Cys Trp Ser Met Tyr Gly Gln Glu Met Thr Ser Gly Leu Asp Lys
85 90 95

cat ggt ggc agt gaa atg ctc caa aca cat ttc tac acc gat aac aag 336
His Gly Gly Ser Glu Met Leu Gln Thr His Phe Tyr Thr Asp Asn Lys
100 105 110

aaa tat gct gta aat gat gtt tcc ttc tca atc cct gcc gcc tct gaa 384
Lys Tyr Ala Val Asn Asp Val Ser Phe Ser Ile Pro Ala Ala Ser Glu
115 120 125

ttt gct gac ctt agt aac atc atc aat aaa tta cta aag gac aaa aat 432

Phe	Ala	Asp	Leu	Ser	Asn	Ile	Ile	Asn	Lys	Leu	Leu	Lys	Asp	Lys	Asn		
130						135				140							
gag ttc cac aaa cat atg gag ttt tat ttc ctt att aag ggc cag ttt 480																	
Glu	Phe	His	Lys	His	Met	Glu	Phe	Tyr	Phe	Leu	Ile	Lys	Gly	Gln	Phe		
145					150					155					160		
ctg cga atg tcc ttg gtc aaa cac atg gaa ctg gag aac atg tca tca 528																	
Leu	Arg	Met	Ser	Leu	Val	Lys	His	Met	Glu	Leu	Glu	Asn	Met	Ser	Ser		
				165					170					175			
gaa gta gtt gtg gaa ata gaa tat gtg aag tac aca gca ccc cag cca 576																	
Glu	Val	Val	Val	Glu	Ile	Glu	Tyr	Val	Lys	Tyr	Thr	Ala	Pro	Gln	Pro		
				180				185					190				
gag caa tgc atg ttc cat gat gac tgg atc ctt tca gtt aaa ggg gca 624																	
Glu	Gln	Cys	Met	Phe	His	Asp	Asp	Trp	Ile	Leu	Ser	Val	Lys	Gly	Ala		
		195					200					205					
aag gaa tgg atc ttg act ggt tct tat gat aag acc tct caa atc cgg 672																	
Lys	Glu	Trp	Ile	Leu	Thr	Gly	Ser	Tyr	Asp	Lys	Thr	Ser	Gln	Ile	Arg		
	210					215				220							
tcc ttg gaa aga aag tca ata atg aca att gtt gga cat agg gat gtc 720																	
Ser	Leu	Glu	Arg	Lys	Ser	Ile	Met	Thr	Ile	Val	Gly	His	Arg	Asp	Val		
225					230					235					240		
tta aaa gat gtg gcc tgg gcc aaa aaa aaa gat agt ttg tct tgc tta 768																	
Leu	Lys	Asp	Val	Ala	Trp	Ala	Lys	Lys	Lys	Asp	Ser	Leu	Ser	Cys	Leu		
				245				250						255			
ttt gtg agt gcc tct atg gat cca act att ctc tta tgg gag tgg aat 816																	
Phe	Val	Ser	Ala	Ser	Met	Asp	Pro	Thr	Ile	Leu	Leu	Trp	Glu	Trp	Asn		
			260				265					270					
aga gag aaa caa agt gaa agc ccg acc gtg ctg cag agg tca tgc tgg 864																	
Arg	Glu	Lys	Gln	Ser	Glu	Ser	Pro	Thr	Val	Leu	Gln	Arg	Ser	Cys	Trp		
		275					280					285					
aag tgc aga gtc tat agc tgt tga 888																	
Lys	Cys	Arg	Val	Tyr	Ser	Cys	*										
	290					295											

<210> 324
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 324

Met	Arg	Leu	His	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Cys	Gly	Ala	Gly	Thr
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			20					25					30		
Asn	Gly	Asn	Gly	Ser	Leu	Glu	Leu	Pro	Gly	Ala	Val	Pro	Gly	Cys	Val
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His	Ser	Ala	Leu	Phe	Gln	Gln	Gly	Leu	Ile	Gln	Val	Thr	Leu	Leu	Cys
			50			55					60				
Glu	Gly	Tyr	Ser	Ala	Gly	Glu	Trp	Lys	Pro	Gly	Asp	Gln	Pro	Gly	Asp
65					70				75					80	
Tyr	Cys	Trp	Ser	Met	Tyr	Gly	Gln	Glu	Met	Thr	Ser	Gly	Leu	Asp	Lys
				85					90					95	
His	Gly	Gly	Ser	Glu	Met	Leu	Gln	Thr	His	Phe	Tyr	Thr	Asp	Asn	Lys
			100				105						110		
Lys	Tyr	Ala	Val	Asn	Asp	Val	Ser	Phe	Ser	Ile	Pro	Ala	Ala	Ser	Glu
		115				120						125			
Phe	Ala	Asp	Leu	Ser	Asn	Ile	Ile	Asn	Lys	Leu	Leu	Lys	Asp	Lys	Asn
		130				135						140			
Glu	Phe	His	Lys	His	Met	Glu	Phe	Tyr	Phe	Leu	Ile	Lys	Gly	Gln	Phe
145					150				155						160
Leu	Arg	Met	Ser	Leu	Val	Lys	His	Met	Glu	Leu	Glu	Asn	Met	Ser	Ser
				165				170					175		
Glu	Val	Val	Val	Glu	Ile	Glu	Tyr	Val	Lys	Tyr	Thr	Ala	Pro	Gln	Pro
			180					185					190		
Glu	Gln	Cys	Met	Phe	His	Asp	Asp	Trp	Ile	Leu	Ser	Val	Lys	Gly	Ala
		195				200						205			
Lys	Glu	Trp	Ile	Leu	Thr	Gly	Ser	Tyr	Asp	Lys	Thr	Ser	Gln	Ile	Arg
		210				215					220				
Ser	Leu	Glu	Arg	Lys	Ser	Ile	Met	Thr	Ile	Val	Gly	His	Arg	Asp	Val
225				230						235					240
Leu	Lys	Asp	Val	Ala	Trp	Ala	Lys	Lys	Lys	Asp	Ser	Leu	Ser	Cys	Leu
				245				250						255	
Phe	Val	Ser	Ala	Ser	Met	Asp	Pro	Thr	Ile	Leu	Leu	Trp	Glu	Trp	Asn
			260					265					270		
Arg	Glu	Lys	Gln	Ser	Glu	Ser	Pro	Thr	Val	Leu	Gln	Arg	Ser	Cys	Trp
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Lys Cys Arg Val Tyr Ser Cys
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<211> 549
<212> DNA
<213> Homo sapiens

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ctg ctt ttt att cta tcc gtg ctg gca gct gat gag atg atg ccc acc 96
Leu Leu Phe Ile Leu Ser Val Leu Ala Ala Asp Glu Met Met Pro Thr
20 25 30

cag att gag gct act att acc ttc ttg ctt gtc acg ttg ctc att tac 144
Gln Ile Glu Ala Thr Ile Thr Phe Leu Leu Val Thr Leu Leu Ile Tyr
35 40 45

tcc tca ggg cca gct agg tgc ctg gag tct ccc ctg aaa gaa ctc aag 192
Ser Ser Gly Pro Ala Arg Cys Leu Glu Ser Pro Leu Lys Glu Leu Lys
50 55 60

att ttc ctt tat ttt cat gct cag cgc ggg ggt gcg gca gag gtc cct 240
Ile Phe Leu Tyr Phe His Ala Gln Arg Gly Gly Ala Ala Glu Val Pro
65 70 75 80

gct ctg tct cac tgg gac tat caa gtg tct ggt aca gaa aat aga gca 288
Ala Leu Ser His Trp Asp Tyr Gln Val Ser Gly Thr Glu Asn Arg Ala
85 90 95

act caa tgc agt tgc cgg ttt cag agc att ctt gaa ttg atc gtg aaa 336
Thr Gln Cys Ser Cys Arg Phe Gln Ser Ile Leu Glu Leu Ile Val Lys
100 105 110

cag ctt tcc agg tgc gat cgt ata aag gat cat tgg cag ctg tgc agc 384
Gln Leu Ser Arg Cys Asp Arg Ile Lys Asp His Trp Gln Leu Cys Ser

115	120	125	
ttg tca gct agc tgc aga aac cca ggt gtc atg ctg aca gct tca gtg			432
Leu Ser Ala Ser Cys Arg Asn Pro Gly Val Met Leu Thr Ala Ser Val			
130	135	140	
tta ata gcc ttt cag act tgg aga gcc agc atc cga cat aaa aat gat			480
Leu Ile Ala Phe Gln Thr Trp Arg Ala Ser Ile Arg His Lys Asn Asp			
145	150	155	160
agt ctt ata gag ttt gtt aat cag ctc tca aca ctg tgt aag aat aga			528
Ser Leu Ile Glu Phe Val Asn Gln Leu Ser Thr Leu Cys Lys Asn Arg			
165	170	175	
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Pro Leu Asp Arg Leu Leu *			
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<400> 326

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Gln Ile Glu Ala Thr Ile Thr Phe Leu Leu Val Thr Leu Leu Ile Tyr			
35	40	45	
Ser Ser Gly Pro Ala Arg Cys Leu Glu Ser Pro Leu Lys Glu Leu Lys			
50	55	60	
Ile Phe Leu Tyr Phe His Ala Gln Arg Gly Gly Ala Ala Glu Val Pro			
65	70	75	80
Ala Leu Ser His Trp Asp Tyr Gln Val Ser Gly Thr Glu Asn Arg Ala			
85	90	95	
Thr Gln Cys Ser Cys Arg Phe Gln Ser Ile Leu Glu Leu Ile Val Lys			
100	105	110	
Gln Leu Ser Arg Cys Asp Arg Ile Lys Asp His Trp Gln Leu Cys Ser			
115	120	125	
Leu Ser Ala Ser Cys Arg Asn Pro Gly Val Met Leu Thr Ala Ser Val			
130	135	140	

Leu Ile Ala Phe Gln Thr Trp Arg Ala Ser Ile Arg His Lys Asn Asp
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 Ser Leu Ile Glu Phe Val Asn Gln Leu Ser Thr Leu Cys Lys Asn Arg
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 Pro Leu Asp Arg Leu Leu
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ttg atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg 96
 Leu Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu
 20 25 30

gcc ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca 144
 Ala Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro
 35 40 45

gtg ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg 192
 Val Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val
 50 55 60

gga gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac 240
 Gly Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp
 65 70 75 80

gtg atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg 288
 Val Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro
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ctg ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg cgg gag cag ggc 336
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 Ala Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro
 35 40 45
 Val Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val
 50 55 60
 Gly Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp
 65 70 75 80
 Val Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro
 85 90 95
 Leu Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly
 100 105 110
 Thr Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly
 115 120 125
 Pro Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro
 130 135 140
 Arg Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly
 145 150 155 160
 Asp Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg
 165 170 175
 Asp Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu
 180 185 190
 Ala Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg
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 Leu Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp
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 Leu Gly
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<213> Artificial Sequence

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